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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acatatgtgcgctgcctcaa.....tgctcccagatgctgttccc 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822.840 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 7 7 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
294 294 294 294 292.4 292.4 292.4 291.6 204.4 151.8	Score
100.0 100.0 100.0 100.0 99.5 82.2 82.2 69.5 51.6	Query
294 1383 2817 2817 2817 1383 1383 1383 1542 1542 31000 31000	Query Match Length DB
14 10 14 10 10 10 10	DB.
US-10-001-254-5 US-10-001-254-15 US-09-966-451-3 US-10-001-254-27 US-10-630-399-3 US-09-759-595-2 US-09-759-595-2 US-09-759-595-4 US-09-759-595-4 US-09-759-595-4 US-09-966-451-10 US-10-630-399-10	ID
Sequence 5, Appli Sequence 15, Appl Sequence 27, Appli Sequence 27, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 149, Appli Sequence 4, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli	Description

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33.2	33.4	•			33.6	•	•	33.8		•	33.8	34.4	34.6	35	. 36	36	37	37	39.6	40.4	40.4	40.4	40.4	40.4		42.6	42.6		104.8	•	137.6	٠
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14	18	16	8	10	18	16	15	16	10	10	16	18	18	16	11	9	13	18	18	11	10	9	9		18	18	18	13	11	16	16	4
US-10-198-846-7068	US-10-723-860-5341	US-10-158-844-90	US-08-961-527-90	US-09-769-787-287	US-10-425-115-181981	US-10-425-114-13505	US-10-205-220-1	US-10-251-668-2	US-09-960-858-2	US-09-960-870-2	US-10-282-122A-27393	US-10-723-860-4422	US-10-425-115-154005	US-10-282-122A-40657	US-09-938-842A-4518	US-09-938-842A-4518	US-10-087-192-1831	US-10-674-124A-9403	US-10-468-488-12	US-09-893-820-51	US-09-900-797-51	US-09-903-012-51	US-09-887-586A-51	บร-09-895-752-51	US-10-357-930-29035	US-10-357-930-23166	US-10-422-522-27	US-10-087-192-1000	US-09-969-034-428	US-10-085-783A-26096		00-10-001-004-00
	Sequence 5341, Ap	Sequence 90, Appl	Sequence 90, Appl	Sequence 287, App	. Sequence 181981,	13	Ļ		'n		27393,	Sequence 4422, Ap		40657,	•	4518, /		9				Ģ	5	.51		231	27,	100	Sequence 428, App	Sequence 26096, A	•	

ALIGNMENTS

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US-10-001-254-5
; Sequence 5, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Powntowski, Krzysztof
APPLICANT: Lee, Sug Hyung
APPLICANT: Lee, Sug Hyung
APPLICANT: Lee, Sug Hyung
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Roth, Wilfred
APPLICANT: Roth, Wilfred
CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
; NUMBER: OP 55
LENGTH: 294
TYPE: DNA
ORGANISM: Homo Bapien
FEATURE:
NAME/KEY: CDS
LENGTH: 294
US-10-001-254-5

Query Match
D10.0%; Score 294; DB 14; Length 294;
Best Local Similarity 100.0%; Pred. No. 5.4e-75;
Matches 294; Conservative 0; Mismatches 0; Gaps
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; NAME/KEY: CDS
; LOCATION: (1)...(1380)
US-10-001-254-15
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US-10-001-254-15
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SOFTWARE: FastSEQ for Windows Version
LEMETER - ***
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-629
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, John C. APPLICANT: Godzik, Adam APPLICANT: Pawlowski, K.
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1383
                                               181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                        121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
241 ATCCAAAATGAATTTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
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                                                                                                                                                                                                                                                                                       Similarity
                                                                                    AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAAACTGGAAAAAGTCCCCACTTCT
                                                                                                                                             ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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Fiorentino, Loredana
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Roth, Wilfred
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100.0%; Pred. No. 1.1e-74;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             Length 1383;
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APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Stemmer-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Pro
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-01-254-27
is Sequence 27, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
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APPLICANT: Godzik, Adam
APPLICANT: BawLowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-966-451-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-966-451-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS)
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09966451 Publication No. US20030087856A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTGTGGATCTTTTG
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; LOCATION: (50)...(1429)
US-10-001-254-27
                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (50)...(1432)
US-10-630-399-3
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US-10-630-399-3
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; SEQ ID NO 3
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10630399 Publication No. US20040019009A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 294; DB 14; Best Local Similarity 100.0%; Pred. No. 1.5e-74; Matches 294; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/10/630,399
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/9/966,451
PRIOR FILING DATE: 2001-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                             194
                                                                                                                                                                                                 294;
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                                                AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAAGTCCCCACTTCT 180
                                                                                  ACATATGTGCGCTGCCTCAATGTTGGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                           ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
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                                                                                                                                                                                                                           Length 2817;
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LENGTH: 1383
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APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Tilarik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Me
FILE REFERENCE: 018791-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
Sequence 2, Application US/09759595
Publication No. US20030059916A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Tilarik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods
FILE REFERENCE: 018791-003910US
CURRENT APPLICATION UNMBER: US/19/759,595
CURRENT FILING DATE: 2001-01-13
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LOCATION: (1)..(1383)
OTHER INFORMATION: human IRAK-4
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ORGANISM: Homo sapiens
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OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
OTHER INFORMATION: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGCTGGTGATCTTGTGGATCTTTTG
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99.7%;
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Pred. No. 3.2e-74;
0; Mismatches 1;
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APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
ITITLE OF INVENTION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0.
SEQ ID NO 149
LENGTH: 501
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(501)
OTHER INFORMATION: n = A,T,C or G
US-09-833-790-149

NO 24: SCOTE 241.6; DB 9; Length 501
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US-09-833-790-149
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; LOCATION: (1)..(1383)
CTHER INFORMATION: human IRAK-4
US-09-759-595-2
   Query Match
Best Local Similarity
Matches 288; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 149, Application US/09833790 Patent No. US20020068288A1
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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   Conservative
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                 82.2%;
97.3%;
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Pred. No. 3.2e-74;
0; Mismatches 1;
Score 241.6; DB 9;
Pred. No. 1.1e-59;
0; Mismatches 4;
                                Length 501;
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APPLICANT: Wesche, Holger

APPLICANT: Li, Shyun

APPLICANT: Tularik Inc.

FITTLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 018781-003910US

CURRENT APPLICATION NUMBER: US/99/795,595

CURRENT FLING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR FILING DATE: 2000-01-13

NUMBER OF 502 ID NOS: 7

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 4

LENGTH: 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4); OTHER INFORMATION: CDNA
; NAME/KEY: CDS
; LOCATION: (163)...(1542)
; OTHER INFORMATION: murine IRAK-4
US-09-795-595-4
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US-09-795-595-4
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Publication No. US20020039423A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 238; Conserv
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    427
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                                                                                                                                                                                                                                                                     247 CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAGATAC
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                            ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                     GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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81.0%;
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Pred. No. 1.1e-48;
0; Mismatches 56;
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APPLICANT: Wesche, Holger

APPLICANT: Li, Shyun

APPLICANT: Tularik Inc.

APPLICANT: Tularik Inc.

FILE REFERENCE: 018781-003910US

FILE REFERENCE: 018781-003910US

CURRENT APPLICATION NUMBER: US/09/759,595

CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENCTH: 1542
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US-09-966-451-10
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                                                                                                                                                                                                                                       Sequence 10, Application US/09966451 Publication No. US20030087856A1 GENERAL INFORMATION:
                                                                          NUMBER OF SEQ ID
SEQ ID NO 10
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Best Local Similarity
                                                                                                              APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (163)...(1542)
OTHER INFORMATION: murine IRAK-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus sp.
        TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:
                                                       ENGTH: 31000
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81.0%;
                                                                                               2001-09-28
88
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Pred. No. 1.1e-48;
                                                                                                                                                                              IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Indels
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Sequence 25, Application US/10001254
Publication No. US/20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzák, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
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US-10-630-399-10
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US-10-001-254-25
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CURRENT APPLICATION NUMBER: US/10/630,399
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/09/966,451
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10630399
Publication No. US20040019009A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGAT 242
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                                                                                               Lee, Sug Hyung
Roth, Wilfred
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95.7%;
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95.7%;
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Pred. No. 7.9e-33;
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Pred. No. 7.9e-33;
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US-10-242-535A-26096
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PRIOR PILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR TILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
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Best Local S
Matches 140
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SEQ ID NO 25
LENGTH: 211
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(177)
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26096, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
                                                                                                                                                                                                   Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 26096
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                              ENGTH: 470
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Pred. No. 1.5e-29;
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Sequence 26096, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
APPLICANT: Liew, C.C.
FILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: Patentin version 3.2

SEQ ID NO 26096

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Search completed: January 12, 2005, 07:07:01
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                                                                                                                                121 AATCAGTTTCACATAAGGAGATTT 144
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Pred. No. 1.5e-29;
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Total number of hits satisfying chosen parameters:
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Sequence 10, Appli
Sequence 11, Appli
Sequence 51, Appli
Sequence 1549, Appli
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ALIGNMENTS	4 US-09-134-000C-1031 4 US-09-976-594-423 4 US-09-427-501-1	4 US-09-248-796A-6765	2 US-08-545-745-1	1 US-08-403-866-11	4 US-09-710-279-3929	4 US-09-710-279-3998	4 US-09-710-279-3337	4 US-09-621-976-2813	4 US-09-692-570-1	4 US-08-916-421B-1	4 US-09-710-279-3771	4 US-09-620-312D-120	3 US-09-134-001C-1614	4 US-09-710-279-2681	4 US-08-781-986A-37
	Sequence 1031, Ap Sequence 423, App Sequence 1, Appli	Sequence 6765, Ap	. ب	Sequence 11, Appl	Sequence 3929, Ap	Sequence 3998, Ap	Sequence 3337, Ap	Sequence 2813, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 3771, Ap	Sequence 120, App	Sequence 1614, Ap	Sequence 2681, Ap	Sequence 37, Appl

APPLICANT: Scanlan, Matthew APPLICANT: Scanlan, Matthew APPLICANT: Scanlan, Matthew APPLICANT: Scanlan, Matthew APPLICANT: Stockert, Elisabeth APPLICANT: Jager, Elke APPLICANT: Jager, Elke APPLICANT: Jager, Elke APPLICANT: Knuth, Alex TITLE OF INVENTION: Renal Cancer Associated Antigens and TITLE OF INVENTION: Uses Therefor FILE REFERENCE: L0461/7051 CURRENT APPLICATION NUMBER: US/09/166,350A CURRENT FILING DATE: 1998-10-05 EARLIER APPLICATION NUMBER: US 09/166,350 EARLIER FILING DATE: 1998-10-05 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 10 LENGTH: 833 TYPE: DNA ORGANISM: Homo sapiens US-09-166-350-10 Query Match 100.0%; Best Local Similarity 100.0%; Matches 294; Conservative 0 GENERAL INFORMATION: Sequence 10, Application US/09166350A Patent No. 6440663 Score 294; DB 4; Pred. No. 1.1e-82;); Mismatches 0;

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181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGGTTGGTGGATCTTTTTG

GTTGGTGATCTTGTGGATCTTTTG

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ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC

121 AATCAGTTTCACATAAGGAGTTTGAAGGCATTACTTCAAACTGGAAAAAGTCCCACTTCT

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AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCCACTTCT

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US-09-966-451-3
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                                                                                                                                                                                                                                                        APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
                                                                                                                          Query Match
Best Local Similarity
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Patent No. 6692959
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APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT FILING DATE: 2001-09-28
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                              FEATURE:
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NAME/KEY: CDS
LOCATION: (50)...(1432)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                      TCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGA 182
                                  TTĀCTTĀČTTTTĀĀĠĠĀĠĀTTTĠĀĀĠĊĀTTĀĊTTĊĀĀĀĊTGĠĀĀĀĀĀĠTĊĊĊĀĊTTĊTĠĀ
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                                                                                                        Conservative
                                                                                                                      51.6%;
95.7%;
                                                                                                   Score 151.8; DB 4;
Pred. No. 2.3e-37;
0; Mismatches 7;
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Pred. No. 1.9e-82;
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                                                                                                                                   Length 31000;
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Sequence 3, Application US/09601091
Patent No. 6342380
GENERAL INFORMATION:
APPLICANT: COLDY, S. M. et al.
TITLE OF INVENTION: Germacrene C Synthase Gerelle REFERENCE: 4630-55758
CURRENT APPLICATION UNMER: US/09/601,091
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: PCT/US99/02133
PRIOR TILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR PILING DATE: 1998-02-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 3
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US-09-601-091-1
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TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (39)..(1685)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Patent No. 6342380
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Pred. No. 0.0064;
0; Mismatches 96;
                                                                                                                                                     Gene
                                                                                                                                                  of Lycopersicon
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RESULT 6
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                                                                                                                                                                                Matches
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Best Local A
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chappell
APPLICANT: No. 646
APPLICANT: Starks,
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
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PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/398,395A CURRENT FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
NAME/KEY: CDS
LOCATION: (32)...(1675)
OTHER INFORMATION: VFNT germacren
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LOCATION: (32)..(1678)
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                                                                                                                                                                                               ocal Similarity
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                                    814 TGCAAGAGACAGGTTGGTTGAGTGTTACTTCTGGATATTAGGAGTGTATTTTGAGCCAAA 873
                                                                       105 TGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGG
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   165 AAAAAGTCCCACTTCTGAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGA 224
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                                                                                                                                                                                98;
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                                                                                                         TCTTGTGGATCTTT 238
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                                                                                                                                                                                Conservative
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FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 2001-06-29
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RESULT 8
US-09-85-752-51
; Sequence 51, Application US/09895752
; Patent No. 6559297
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SEQ ID NO 51
LENGTH: 2024
                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Chappell, Joseph
APPLICANT: No. 65593971, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
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APPLICANT: No. 64953541, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
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LOCATION: (32)...(1675)
OTHER INFORMATION: VFNT
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ORGANISM: Lycopersicon esculentum
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Pred. No. 0.0066;
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Best Local Similarity

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US-09-903-012B-51
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; OTHER INFORMATION: VFNT germacrene C synthase US-09-895-752-51
                                   US-09-903-012B-51
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LENGTH: 2024
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LENGTH: 2024
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Query Match
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                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Starks, Courtney M
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                            SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-04-22
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                                                                                                                TYPE: DNA ORGANISM: Lycopersicon esculentum
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                                                LOCATION: (32)...(1675)
OTHER INFORMATION: VFNT
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                                                                                       NAME/KEY: CDS
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Local Similarity 50.5%;
les 98; Conservative
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FILING DATE: 1999-09-17
APPLICATION NUMBER: 60/100,993
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/130,628
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13.7%;
                                                  germacrene
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Pred. No. 0.0066;
Score 40.4;
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US-09-900-797-51
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; NAME/KEY: CDS
; LOCATION: (32)...(1675)
; OTHER INFORMATION: VFNT germacrene C synthase US-09-900-797-51
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CURRENT APPLICATION NUMBER: US/09/900,797

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US/09/398,395

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/130,628

PRIOR FILING DATE: 1999-04-22

PRIOR APPLICATION NUMBER: 60/150,262

PRIOR APPLICATION NUMBER: 60/150,262

PRIOR APPLICATION NUMBER: 50/150,262

PRIOR FILING DATE: 1999-08-23

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PRIOR FILING DATE: 1999-08-23
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Matches
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SEQ ID NO 51
LENGTH: 2024
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Lycopersicon esculentum
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0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                 Score 40.4; DB 4; Pred. No. 0.0066;
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Mismatches
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US-08-545-528D-1/c
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1549
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APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
Patent No. 6537773
                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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LENGTH: 267
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Patent No. 6605709
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Thereof, and Uses ThereILE REFERENCE: PB193P1
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR ETLING DATE: 1999-04-09
PRIOR ETLING DATE: 1999-04-09
PRIOR ETLING DATE: 1999-04-09
PRIOR SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 580073
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                                                                                                                                                                                              143 TTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTGACTGGGGCA
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CTAACAGTCTTAT 431571
                                       CIGCGAGICITIT 275
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                                                                                                                                                                                                                                          Conservative
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Pred. No. 0.013;
0; Mismatches 38;
                                                                                                                                                                                                                                      Score 33.8; DB 4;
Pred. No. 9;
0; Mismatches 62;
                                                                                                                                                                                                                                      62;
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                                                                                                                                                                                                                                                                              Length 580073;
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RESULT 14
US-08-961-527-90/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-583-110-1653/c
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Sequence 90, App.
Sequence 90, App.
No. 642013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SEQ ID NO 1653
LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Lynn Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1653, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relat:
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Charle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                          PRIOR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                  CITY: Rockville
STATE: Maryland
                                   APPLICATION NUMBER:
                                                                                                                                                         OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                               CLASSIFICATION: 424
                                                                                                                                                                                                   COMPUTER:
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: HOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION UNMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
VUMBER OF SEQ ID NO 236
SEQ ID NO 236
SEQ ID NO 236
SEQ ID NO 236
COGANUSM: Candida albicans
US-09-248-796A-236
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US-09-248-796A-236
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                                                                                                                                                                                                                                                                                         Query Match 11.3%; Score 33.2; DB 4; Length 654; Best Local Similarity 51.3%; Pred. No. 0.74; Matches 77; Conservative 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236, Application US/09248796A Patent No. 6747137
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Best Local Similarity 48.9%;
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
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346 AAGTATGACTCCATTGTTACCAAGGAT 375
                                      205 ACAAATTGCACAGTTGGTGATCTTGTGGAT 234
                                                                                                286 GCAAAATTAATGGAAGATTTAGAAAAGCCAACTTTGGAATACCTAGTTAACAAAGCAGCT 345
                                                                                                                                      145 GAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTTGACTGGGGCACC 204
                                                                                                                                                                                           226 GTAGCAATCAAGACACACGCAGACCGTTTAAGTTTGAATGTAATGCCCATAAAAGAACAT 285
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Search completed: January 12, 2005, 05:40:47 Job time : 90 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       292.94
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Copyright (c) 1993 - 2005 Compugen Ltd.
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BW513167
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AY418792 Pan trog1
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BQ552228 H4014C09-
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ALIGNMENTS

Query Match Best Local Similarity Matches 294; Conser	ORIGIN	FEATURES FEATURES FOURCE	RESULT 1 LOCUS BG164491 LOCUS GENITION 6 DEFINITION 6 ACCESSION BWASTION BW
100.0%; 100.0%; vative 0;	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clome="IMAGE:4452055" /tissue_type="hypernephr /lab_host="HIOB (phage- /lab_host="DIOB (phage- /clome_lib="NIH MGC 89" /note="Organ: kIdney; ve Site_2: Sall; Cloned uni Average insert size 1.3 full-length clones and c Note: this is a NIH_MGC	Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10240 row: d column: 08 High quality sequence stop: 634. Location/Qualifiers 1859	BG164491 BG164491 BG1642026F1 NIH MGC 89 Homo sapiens cDNA clone IMAGE:4452055 5', BG164491 BG164491 BG164491 BG164491 BG164491 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 859) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
Score 294; DB 4; Le Pred. No. 1e-70; Mismatches 0; I	/organism="Homo sapiens" /mol type="mRNA" /mol type="mRNA" /db_xref="Mtaxon:9606" /db_xref="Mtaxon:9606" /clone="IMAGE:4452055" /clone="type="hypernephroma, cell line" /lab host="hype="hypernephroma, cell line" /lab host="hype="hypernephroma, cell line" /lab host="hype="hypernephroma, cell line" /lab host="hype="hypernephroma, cell line" /clone lib="NNH MGC 89" /clone lib="NNH MGC 89" /clone lib="NNH MGC 89" /clone="hype="hypernephroma, cell line" /clone="host="hype="hypernephroma, cell line" /clone="host="hype="hypernephroma, cell line" /clone="host="hype="hypernephroma, cell line" /clone="hype="hypernephroma, cell line" /clone="hype="hypernephroma, cell line" /clone="hype="hypernephroma, cell line" /clone="hype="hype="hypernephroma, cell line" /clone="hype	nail.nih.gov tt: ATCC paration: Life Technologies paration: Life Technologies paration: Life Technologies ayed by: The I.M.A.G.E. Con y: Incyte Genomics, Inc. on: MGC clone distribution i.M.A.G.E. Consortium/LLNL i.M.A.G.E. Consortium/LLNL row: d column: 08 row: d column: 08 tence stop: 634. lence stop: 634.	859 bp mRNA linear EST 06 89 Homo sapiens cDNA clone IMAGE:44520 1194 Chordata; Craniata; Vertebrata; Eutele Primates; Catarrhini; Hominidae; Homo. nci.nih.gov/. of Health, Mammalian Gene Collection (ausberg, Ph.D.
Length 859; Indels 0; Gaps	ine" SPORT6; Site_1: NotI ly; oligo-dT primed. enriched for by Life Technologies	, Inc. sortium (LLNL) information can be at:	bp mRNA linear EST 06-FEB-2001 apiens cDNA clone IMAGB:4452055 5', (Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. (Catarrhini; Gene Collection (MGC) h.D.
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High quality sequence start: 3
High quality sequence stop: 613.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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                                                            /tissue_type='embryonal carcinoma"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/clone_lib="NIH_MGC_61"
/clone_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgtctggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5;
and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5'-CACGGCCATTATGGCC_3 and 3' adaptor
sequence: 5'-CACGGCCATGGCCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
contained inserts by PCR. This library was enriched for
laboratories (Palo Alto, CA). Note: this is a NIH_MGC
1.thraw, "
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I (bases 1 to 821)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                                                                                                                                        cross_match v0.990329.
Plate: TMW8032 row: K column: 2:
Seq primer: GTAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CK459029
CK459029.1 GI:40830310
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923479 MARC 4PIG Sus scrofa cDNA 5', mRNA
ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGTTGTCAGATTTTATTGATCCT
                ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCAAAATGAAITTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                        /clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not /ibrary made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PIG"
                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                              .821
                                                                                  92.9%;
95.6%;
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                                                                Score 273.2; DB 7;
Pred. No. 5.9e-65;
D; Mismatches 13;
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0; Mismatches
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sequence.
                                                                                                 Length 821;
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Sus.
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RESULT 4
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JOURNAL
                                                                                                                      Query Match
Best Local Similarity
Matches 291; Conser
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92
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM124 row: g column: 15
High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF696981
602130160F1 NIH_MGC_56 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 719)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF696981.1 GI:11982389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
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ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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                                                                                                                      Conservative
                                                                                                                                                                                                                                                             /tissue_type="primitive neuroectoderm"
/lab host="DH10B (T1 phage resistant)"
/clome_ilb="NH10B (T1 phage resistant)"
/clome_ilb="nHH0G (T5 phage resistant)"
/clome_ilb="nHH0G (T5 phage resistant)"
/clome_ilb="nHH0G (T5 phage resistant); Site_1:
/note="Organ: bTain; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: bTain; Vector: pDNR-LIB (Clontech); Site_1:
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/site_ilb="nhH0G (T5 phage resistant); Site_1: ggccattatggcc);
/site_ilb="nhH0G (T5 phage resistant); Site_1: ggccattafgccatant); Adaptor sequence: 5'-ATTCTAGAGGCCATGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGGGCCGACATG-dT(30)BN-3'
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/sequence: 5'-ATTCTAGAGGCCGAGCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGAGCGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGAGGCCGGCCGACATG-dT(30)BN-3'
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/sequence: 5'-ATTCTAGGCCGGCGCGCGGCCGACATG-dT(30)BN-3'
/sequence: 5'-ATTCTAGGCCGGCGGCCGACATG-dT(30)BN-3'
/seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                             90.9%;
                                                                                                                      0
                                                                                                                Score 267.2; DB 2;
Pred. No. 2.7e-63;
0; Mismatches 3;
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AUTHORS
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Best Local Similarity
Matches 274; Conserv
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Bos taurus
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12140684
                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 11 row: F column: 7
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, Beltsville Agricultural Research Bddg. 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis of bovine mammary gland EST the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 402)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wand Quackenbush, J.
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BE482619.1
                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases ov v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE482619 402 bp mRNA linear 168463 BARC 5BOV Bos taurus cDNA 5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                              PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                              -minmatch 12 options.
   Conservative
                                                                                         /mol_type="mRNA"
/db_xref="taxon:9913"
/db_bxref="taxon:9913"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="BARC_5BOV"
/clone_Tib="BARC_5BOV"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
/instary_made_from_pooled_mRNA_isolated_from_mammary_tissues_at_eight_physiological,_developmental,_and_disease_states."
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                          organism="Bos taurus"
|mol_type="mRNA"
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                   89.1%;
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 Score 262; DB 2; 1
Pred. No. 6.7e-62;
0; Mismatches 20;
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                                    Length 402
   Indels
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CN788062
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                        Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '/ -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 26 row: 0 column: 07
Seq primer: CCTATTTAGGTGACACTATAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construction and Analysis of a cl
Intestinal Muscle and Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 666)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S.,
Matukumalli, L.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CN788062 666 bp mRNA linear EST 26-MAY-2004 4122347 BARC 8BOV Bos taurus CDNA clone 8BOV_26007 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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CN788062
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                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 666.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3015048604
                                                                                                                                                                                                                                               /mol type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8B0V_26007"
/sex="Female"
                                                            /note="Organ: Intestine; Vector: pCMVSport6.1; Site 1: Not1; Site 2: EcoR1; Normalized cow cDNA intestinal library in pCMVsport6.1, constructed from equimolar mRNA pools derived from 5 sources 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                                                                                                                                                                                          /tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
                                                                                                                                                                             'clone
                                                                                                                                                                                                                                                                                                                                  organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                         . 666
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     89.1%;
                                                                                                                                                                           lib="BARC 8BOV"
                                                     Jejunum,
 Score 262;
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al Tissues of Holstein Cattle
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AUTHORS
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Matches 261;
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                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and orde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1383)
Clark, A.G., Glanowski, S., Nielson, R., Thomas; P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                            Similarity
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AY418791
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ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                    based on alignment.
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                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                gene="IRAK4"
                                                                                                                                                                                                               db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                               locus_tag="HCM6675"
                                                                                                                                                                                                                                                                         . 1383
                                                                                          88.8%;
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                                                                                     Score 261; DB 9;
Pred. No. 1.6e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1383)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
These sequences were made by sequencing them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene trios
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY418792.1 GI:39774752
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14671302
                                                                                                                                                                                          Similarity
AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCCACTTCT
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                                                                   ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                 /gene="IRAK4"
/locus_tag="HCM6675"
                                                                                                                                                                                         87.9%;
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                                                                                                                                                                                         Score 258.4; DB 9; Pred. No. 8.3e-61;
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340084 BARC 5BOV Bos taurus cDNA
BG691069
BG691069.1 GI:13932889
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 100 row: B column: 15
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Quackenbush, J.
Analysis of bovine mammary gland EST and the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, B.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., W
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
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TCCCACTTCTGAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGT
                                                                         TGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAG
                                                                                                                        TATTGATCCTCAAGAAGGATGGAAGAAGTTAGCAGTCGCTATTAAAAAAACCATCTGGTGA
                                                                                                                                                   TATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAAACCATCTGGTGA
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol type="maNn.9913"
/tisue_type="pooled"
/lab host="pH108"
/clone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
/ibrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and diseastates."
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                                                                                                                                                                                                          74.8%;
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                                                                                                                                                                                                           Score 220; DB 4;
Pred. No. 3.2e-50;
                                                                                                                                                                                           Mismatches
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1 ACATATGTGCGCTGCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM151935
BM151935.1 GI:17175815
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313 bp mRNA linear EST 30-NOV-2001
TCBAPIE11457 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens CDNA clone TCBAP1145, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                       / ADD__NUMBER_ DATASET (CATCHAR)
/ Clone lib="Pediatric pre-B cell acute lymphoblastic | Clone lib="Pediatric project=TCBA" | // Clone lib="Yector: lambda pSB; Site 1: BamH; Site 2: ECORI; // PIST STRAND CDNA was primed with an anchored | // XhoI-oligo (dT) primer [5'GGAGGACTCGAGCGCCGAGGAGGAG(T) VN 3'; VAA,C,G; N-A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'GAGAGCTCGAGCAGGAGGAG(T) VN 4'S primed with a BamH1-dC primer [5'AGAGACTCGGAGCGCAATAATAATAATAATAATACT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Magaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev stage="pediatric 2 years"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP1145"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                    69.9%;
                                                                     ٥,
                                                                                    Score 205.4; DB 4; Pred. No. 3.3e-46;
                                                               Mismatches
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Other_ESTs: C0272B01-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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181 GAATTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGTGG 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute of Health National Institutes of Health National Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: C0272 row: B column: 01
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CO272B01-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:CO272B01 IMAGE:30017484 5', mRNA sequence. CA538859
CA538859.1 GI:25080828
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Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y.,
Luo,A. and Ko,M.S.H.
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/db_xref="niaEST:C0272B01-5N"
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/tissue_type="whole embryo including extraembryonic tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                              /clone lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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REFERENCE
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                                                                                                                                                                                                    Contact: Yong Qian
Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Inve, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4014 row: C column: 09
Seg primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 bp mRNA linear EST 20-JUN-2002 H4014C09-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4014C09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Kasembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone set
Genome Res. 12 (12), 1999-2003 (2002)
22354164
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BQ552228.1 GI:21453114
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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                                                                                                                                                                                      quality sequence stop:
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/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H4014C09-5"
/db_xref="taxon:10090"
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                                                                                                                                         Location/Qualifiers
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Pred. No. 6.8
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Best Local
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1 (bases | to 610)

ORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Mateuyama,T., Miyazaki,A., Nomura,K.,
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

LU Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB660378 RIKEN full-length enriched, musculus cDNA clone D430042L21 5', mi
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                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This
clone is among a rearrayed set of 7,407 clones from more
than 20 cDNA libraries."
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with tuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                      GTCCAGATTGAGCTGTTTGCCCCCCCCCACTCTCCTGCTGCCGGATGCCGTTCCC
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/dev_stage="13 days embryo"
/lab_host="DH10B"
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Contact: Vacati
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darninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
RIKEN integrated sequence analysis (RISA) system-384-format
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB613447 RIKEN full-length enriched, 10 day neonate skin musculus cDNA clone 4732482P03 5', mRNA sequence.
BB613447
BB613447.1 GI:16454055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 637)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                /tissue_type="skin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="4732482P03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="mixed"
                                                                                                                                                                                                                                                                                                         .one_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site
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                                                                      mouse tissues. 1st strand
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Query Match
Best Local Similarity
El (bases 1 to 638)

RS Nikaido, I., Gosto, N., Saito, R., Nadachi, J., Bono, H., Kondo, S., Nikaido, I., Ogato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, I.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanayaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sulcana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Watanabe, Y., Hayatsu, N., Hirozane, Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 bp mRNA linear BY721552 RIKEN full-length enriched, adult male c musculus cDNA clone 9330209D03 5', mRNA sequence. BY721552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY721552.1 GI:27134669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCAGATTGAGCTGTTTGCCCCCCCCCCACTCTCCTGCTGCCGGATGCCGTTCCC 486
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Rodentia;
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Pred. No. 7.1e-46;
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Sciurognathi; Muridae; Murinae; Mus.
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RESULT 15 BY721552

RESULT

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Matches

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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Requencer. 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage="adult"
/lab_host="DH10B"
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Search completed; Ja Job time : 1944 secs	d Q	90 QV	B 8	g Sy	g Q	Query Match Best Local Matches 23	ORIGIN
Search completed: January 12, 2005, 05:39:19 Job time : 1944 secs	241 ATCCAAAATGAATTITITGCTCCTGCGAGTCTITTGCTCCCAGATGCTGTTCCC 294	181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGGTATCTTGTGGATCTTTTG 240	121 AATCAGTTTCACATAAGGAGATTTGAAGGATTACTTCAAACTGGAAAAAGTCCCACTTCT 180	61 CAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAAACCATCTGGTGATGATAGATA	1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60	Query Match 69.5%; Score 204.4; DB 6; Length 638; Best Local Similarity 81.0%; Pred. No. 7.1e-46; Matches 238; Conservative 0; Mismatches 56; Indels 0; Gaps 0;	

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P			SUMMAKIBS	
Result		Query	7 23 4 4	3	;	
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4.	294	100.0	1383	σ	AAD40079	•
υ	294	100.0	1383	σ	AAD59061	Human
σ	294	100.0	1668	ហ	AAS76805	-
7	294	100.0	2817	σ	AAD40085	Aad40085 Human IRA
8	294	100.0	2817	σ	AAD59067	Human
9	294	100.0	2817	10	ACC47548	Acc47548 Human IL-
10	292.4	99.5	1383	Ç	AAD10197	Aad10197 Human int
11	241.6	82.2	501	σ	AAS61608	Aas61608 Lung smal
12	204.4	69.5	1542	v	AAD10198	Aad10198 Mouse int
13	151.8	51.6	31000	10	ACC47549	Acc47549 Human DNA
14	150.4	51.2	405	Ŋ	AAS76803	Aas76803 DNA encod
15	137.6	46.8	211	σ	AAD40084	Aad40084 Human IRA
16	137.6	46.8	211	σ	AAD59066	Aad59066 Human IRA
17	137.6	46.8	415	vi	AAS76802	Aas76802 DNA encod
18	137.6	46.8	2213	4	AAH13798	Aah13798 Human cDN
19	137.6	46.8	2432	12	ADE28369	Ade28369 Human KPP
20	104.8	35.6	408	6	ABQ56733	Abq56733 Human col
21	42.6	14.5	2378	ហ	ABV29017	Abv29017 Human pro

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22
33.6	33.6	33.6	33.8	33.8	33.8	33.8	33.8	33.8	34.2	34.4	34.4	34.4	35	35.2	35.6	36	36	38.2	39.6	40.4	40.4	40.4	42.6
11.4	11.4	11.4	11.5	11.5	11.5	11.5	11.5				11.7	11.7	11.9	12.0	12.1	12.2	12.2	13.0	13.5	13.7	13.7	13.7	14.5
2393	2349	831	110000	22684	22684	22684	3879	3744	107159	131673	110000	110000	2703	14041	2000	2000	739	267	628	2024	2024	1879	2378
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AAV52223	AAA05514	ABX08179	AAT58840_4	ADN48939	ACC69134	AAD63504	ACA39523	AAA70149	ADL13431	ADQ21602	ADB12064_05	ADB12064_04	ACA52787	AAH48024	ADA72207	ABZ16713	ADD45156	ADF01264	AAH87656	AAA38935	AAX89866	AAX89865	ABV23177
Aav52223 Streptoco	Aaa05514 Streptoco	Abx08179 S. pneumo	Continuation (5 of	Adn48939 Mycoplasm	Acc69134 Mycoplasm	Aad63504 Mycoplasm	Aca39523 Prokaryot	Aaa70149 Plasmodiu	Adl13431 Human thy	Adq21602 Human sof	Continuation (6 of	Continuation (5 of	Aca52787 Prokaryot	Aah48024 Internal	Ada72207 Rice gene	Abz16713 Arabidops	Add45156 Human gen	Adf01264 Bacterial	Aah87656 Peppermin	Aaa38935 Tomato ge	Aax89866 L. escule	Aax89865 L. escule	Abv23177 Human pro

ALIGNMENTS

RESULT 1
AAD40074
ID AAD4
XX AAD4
XX AAD4
XX AAD4
XX AAD4
XX Huma
XX Huma
XX Huma
XX Infl
XX Inmu
XX I Human; death domain; DD; death effector domain; DED; Chlamydia infection; MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss. Human IRAK4 DD (death domain) cDNA. 22-OCT-2002 (first entry) AAD40074; WO200240680-A2. Homo sapiens. AAD40074 standard; cDNA; 294 BP. /*tag= a /product= "Human IRAK4 DD" /note= "No start and stop codon" /partial Location/Qualifiers

23-MAY-2002.

17-NOV-2000; 2000US-00715893. 29-JUN-2001; 2001US-0301889P. (BURN-) BURNHAM INST

15-NOV-2001; 2001WO-US044844.

Reed JC, Godzik A, Stenner-Liewen F; Pawlowski K, Fiorentino L, Lee SH, Roth Ξ

WPI; 2002-500222/53. P-PSDB; AAB24854.

New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation,

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RESULT 2
AAD59056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention comparison of the invention comparison of the invention of the useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC commander of the domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NB-DARC detecting the association of the domain and the candidate binding agent and compared to the condidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass compared to the stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. pneumoniae, and C. psittaci or a nucleic acid encoding the cinvention is useful for modulating the activity of oncogenic proteins, the convention is useful for detecting a Chlamydia infection. The convention is useful for detecting a Chlamydia infection. The convention is useful for modulating the activity of oncogenic proteins, for treating bacterial infections by modulating the activity of bacterial for conventions. The protein and antibody specific for it are useful for sepsis, autoimmunity, allograft rejection and other diseases. The protein substituted of the coll division, inflammatory diseases such as sepsis, fibrosis, through antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA convention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA convention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA convention is useful for the convention of the present sequence is human IRAK4 DD cDNA conventions.
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Best Local (
Human; death Domain; DD; death effector domain; DED; cell proliferation Chlamydia trachomatis death domain containing protein; fibrosis; sepsineural growth factor receptor interacting death domain; cell adhesion; neural growth factor receptor interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CT vasorras; beniqu prostatic hypertrophy; antibacterial; NII
                                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                    AAD59056;
                                                                                                                                                                                                                                                                                        AAD59056 standard; cDNA; 294
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Pred. No. 1.4e-77;
; Mismatches 0;
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                                                                                             cell proliferation;
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Query Match Best Local Similarity Matches 294; Conserv

100.0%; Score 294; DB 6 llarity 100.0%; Pred. No. 1.4e-7 Conservative 0; Mismatches

0 Gaps

<u>,</u>

Sequence

294

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c;

62

G; 93 T;

0 U; 0 DB 6;

Other; Length 294;

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CC The present invention provides novel death Domain (DD) and death effector CC domain (DED) proteins and nucleic acids encoding them. The invention also CC provides death domain containing protein such as Chlamydia trachomatis CC death domain containing protein such as Chlamydia trachomatis CC receptor interacting death domain (CTDD) DD and neural growth factor CC receptor interacting death domain (NDD) DD. The invention is useful for CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate CC binding agent and identifying an effective agent (e.g. protein or drug) that binds the DD, DED or NB-ARC domain. The invention is also useful for CC that binds the DD, DED or NB-ARC domain. The invention is also useful for CC that binds the DC DED or NB-ARC domain. The invention is also useful for CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are CC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are cuseful for discovery of drugs that suppress infection, autoimmunity, inflammation, allograft rejection, sepsis and other diseases. CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, allograft rejection, sepsis, keratinocyte inflammatory hyperplasia, keloid, benign prostatic hypertrophy, fibrosis, confidence of the proteins and smooth muscle cell proliferation in arteries cfollowing balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human ccc interleukin-l receptor-associated kinase (IRAK)-4 DD CDMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 33-34; 99pp;
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17-NOV-2000; 2000US-0367360P.
29-JUN-2001; 2001US-0301889P.
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(FIOR/)
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DB; AAE38897.
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) ROTH W.
) STENNER-LIEWEN I
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GODZIK A.
PAWLOWSKI K.
FIORENTINO L.
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iewen F;
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/product= "Human IRAK4 DD
/note= "No start and stop
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                AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated wis abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the mucleic acid molecule or expression product fragment) complexed with a human leukocyte antigen (HLA) molecule and determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder
                                                                                                                                                                                                                                                                                                                                                             Preventing, diagnosing and/or treating disorders associated expression of human cancer associated antigens.
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05-OCT-1998;
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Best Local
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                                                                                                                                                                                                                                                                                                                      Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
           Claim 19; Page 180-182;
                              New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other diseas
                                                                                                                                                                                                                                                                                                                                                                                                                              AAD40079;
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                                                                                                      Reed JC, Godzik A, Stenner-Liewen F;
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29-JUN-2001;
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2001US-0301889P.
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                                                                                                                                                                                                                                                 /*tag= a
/product= "Human IRAK4"
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                        . 1383
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                                                                                                                 Pawlowski
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          209pp;
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           English
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RESULT 5
AAD59061
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Best Local
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               Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
                                                                                                                                                                                                                                                                            Human IRAK4 full length gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD59061 standard; cDNA; 1383
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interleukin-1 receptor-associated kinase;
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Pred. No. 2
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61 25

ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTAATCGT 294;

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Indels

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120

Similarity

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The present invention provides novel death Domain (DD) and death effector CC domain (DED) proteins and nucleic acids encoding them. The invention also CC death domain containing protein such as Chlamydia trachomatis CC death domain containing protein (CTDD) DD and neural growth factor CC receptor-interacting death domain (NIDD) DD. The invention is useful for CC identifying a binding agent (e.g. protein or drug) that binds a DD. DED CC or NB-ARC domain from DAP3. IRAK4. CTDD, DED or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that binds the DD, DED or NB-ARC domain. The invention is also useful for CC that binds the DD, DED or NB-ARC domain. The invention is also useful for cell proliferation, cell stress responses, responses to microbial CC infection and B cell immunoglobulin class switching. DDs, DED and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allograft rejection, sepsis and other diseases. CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angloplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human cCC interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
   Query Match
Best Local S
Matches 294
                                                                       Sequence 1383 BP; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 10A; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-500222/53.
P-PSDB; AAE38902.
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17-NOV-2000; 2000US-0367360P
29-JUN-2001; 2001US-0301889P
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) GODZIK A.
) GODZIK K.
) PANLOWSKI K.
) FIORENTINO L.
) LEE S H.
) ROTH W.
) STENNER-LIEWEN F
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iewen F;
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                100.0%;
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Score 294; I
Pred. No. 2.3
); Mismatches
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                                                                G; 394 T; 0 U; 0 Other;
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                1; DB 6;
2.3e-77;
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                                 Length 1383;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypuptide in tissue, as molecular weight markers and as a food gupplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders (II) ving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. Als64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained CC electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 12609; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                 Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
           New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other diseas
                                                                                                                                                        17-NOV-2000;
29-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Human IRAK4 gene
                                                                                               Stenner-Liewen
                                                                                                          Reed JC,
                                                                                                                                                                                           15-NOV-2001; 2001WO-US044844
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                                                            P-PSDB;
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                                                            2002-500222/53.
DB; AAE24865.
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2001US-0301889P
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                                                                                                           Pawlowski
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Pred. No. 2.4e-77;
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Best Local Simi
Matches 294;
cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
                                                                                              Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTDD,
                                                                                                                                                                                                                                                                                        Human IRAK4 full length gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTGTGGATCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 294; DB 6;
Pred. No. 2.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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밁 8

ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60

133

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Query Match Best Local

Local

Similarity

100.0%;

Score 294; DB b; Pred. No. 2.9e-77;

Conservative

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CC domain (DED) proteins and nucleic acids encoding them. The invention also CC provides death domain containing protein such as Chlamydia trachomatis CC death domain containing protein such as Chlamydia trachomatis CC death domain containing protein such as Chlamydia trachomatis CC death domain containing protein such as Chlamydia trachomatis CC death for interacting death domain (NIDD) DD and neural growth factor CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED or NIDD with a candidate CC binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein or drug) CC that modulates the DP, DED or NB-ARC domain. The invention is also useful for CC infection and B cell immunoglobulin class switching, cell adhesion, CC inflating and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are CC useful for discovery of drugs that suppress infection, autoimmunity, CC inflammation, allograft rejection, sepsis and other diseases. CDD, DED or NB-ARC domain proteins are used to treat infection, altergy, hyperplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC following balloon angioplasty (restenosis). The invention is also used in the classic interleukin-1 receptor-associated kinase (IRAK)-4 full length gene
         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 51-53; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides novel death Domain (DD) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stenner-Liewen
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(GODZ/)
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17-NOV-2000; 2000US-0367360P.
29-JUN-2001; 2001US-0301889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keloid; interleukin-1 receptor-associated kinase; IRAK; gene;
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FIORENTINO L.
LEE S H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REED J
GODZIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROTH W.
STENNER-LIEWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godzik A,
iewen F;
     BP; 912 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human IRAK4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pawlowski K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
     547 C;
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586 G; 772 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                      death effector invention also
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RESULT 9
ACC47548
                  The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (II-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding II-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with II-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides for modulating II-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
  prophylaxis, or as re
represents the human
                                                                                                                                                                                                                                                                                                                                  Example 13; Page 80-83; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Freier SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC.
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/*tag= a
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  receptor-associated kinase-4
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encoding sequence
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WPI; 2001-451860/48 P-PSDB; AAE05398.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                         Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II, antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; behoet's syndrome; ankylosing spondylitis; II-1 receptor/Toll receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD10197 standard; cDNA; 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                     Wesche H,
                                                                                       13-JAN-2000;
                                                                                                                 12-JAN-2001; 2001WO-US001171.
                                                                                                                                                                  WO200151641-A1
                                                                                                                                                                                                                                                                                 sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
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Pred. No. 2.9e-77;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc associated kinase (IRAK)-4. IRAK associate with activated II-1, II-18 and conther receptors and act to transduce signals originating from the cother receptors and act to transduce signals originating from the cartivated receptors, ultimately leading to a variety of downstream cffects such as muclear factor (NP)-kappaB activation. The IRAK-4 cc inhibitors are useful for treating inflammatory diseases such as cc pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (opp), cc disease syndrome (ARDS), chronic obstructive pulmonary disease (e.g., cc allergic rhinitis), transplant rejection, autoimmune disease (e.g., cd diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cc cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 cc psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic cd ermatitis), inflammatory bowel disease (e.g., Crohn's disease), CD14 cresulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transduction of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman transgenic animal which is useful for testing the function of combuman testivates of the cell. IRAK-4 is used to create a conditions. IRAK-4 sequences combuman testivates and conditions and conditions and conditions and conditions.
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Best Local S
Matches 293
             Lung small cell carcinoma antigen, cDNA #149.
                                                             29-JAN-2002
                                                                                                                                           AAS61608
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                                                                                                                                           standard;
                                                                                                                                                                                                                                                               ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTTCCC
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                                                      (first entry)
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                                                                                                                                           CDNA;
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 292.4; DB Pred. No. 6.9e-77 O; Mismatches
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Best Local Similarity
Matches 288; Conserv
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21-JUN-2000; 2000US-0213361P.
01-SEP-2000; 2000US-0229763P.
05-SEP-2000; 2000US-0230629P.
14-SEP-2000; 2000US-0232565P.
19-DEC-2000; 2000US-0257037P.
08-JAN-2001; 2001US-0260796P.
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Yung tumor polynucleotide and polypeptides useful in therapy and
diagnosis of cancer especially lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010896/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lodes MJ, Wang T, Mohamath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; antitumour; lung small cell cancer antigen; tumour; lung cancer; ss.
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                    239
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                                                                                                                                                                                                                                                                                                                                                                                 1; Page 174; 295pp; English
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          TGATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
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TGATCCAAAATGAA-TTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                 AATCAAGTTTCACATAAGGAGATTTGAAGCATT-CTTCAAACTGGAAAAAGTCCCACTTC
                                                                              AATC-AGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTC
                                 TTGAATACTGTTTGACTGGGGGGCACCACAAATTGGACAGTTGGTGATCTTGTGGATCTTT
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                                                                                                                                                                                                            501 BP;
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nilarity 97.3%;
Conservative
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                                                                                                                                                                       Score 241.6;
Pred. No. 7e-6
0; Mismatches
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                                                                                                                                                                                        Length 501;
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The present sequence is a cDNA encoding mouse interleukin (II)-1 receptor CC associated kinase (IRAK)-4. IRAK associate with activated II-1, II-18 and CC other receptors and act to transduce signals originating from the CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as cC epidenary diseases and diseases of the airway (e.g., adult respiratory CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g., CC inhumatoid arthritis, systemic lupus crythematosus, multiple sclerosis or CC disbetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of CC cardiovascular diseases (e.g., neurodegenerative disease), CD14 CC mediated sepsis, non-CD14 mediated sepsis, osteoparthritis, atopic CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and content of the court of the court of the cardiovascular and court of the skin (e.g., rash, contact dermatitis, atopic court of the court of the cardiovascular and court of the cardiovascular of the skin (e.g., rash, contact dermatitis, atopic court of the cardiovascular of the skin (e.g., rash, contact dermatitis, atopic court of the cardiovascular of the cardiovascular and the cardiovascular of the cardiovascular of the cardiovascular of the cardiovascular of the skin (e.g., rash, contact dermatitis, atopic court of the cardiovascular of the 
dermatitis), inflammatory power usesses (v.5), spondylitis, gout, ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, ulcerative colitis, Behcet's syndrome, ankylosing spondylitis, gout, ulcerative colitis, and conditions. The inhibitors of sarcoidosis and ophthalmic diseases and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; II-1 receptor/Toll receptor; sarcoidosis; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; neuroprotective; chronic cou
adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARD
interstitial lung disease; allergic rhinitis; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 26; Fig 4; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma,
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1. .1542
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Example 15; Page 85-102; 119pp; English

New antisense oligonucleotides for modulating IL-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying treating e.g. cancer (e.g. renal cancer), inflammatory disease or an

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WPI; 2003-363256/34.

28-SEP-2001;

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Freier PHARM INC. 2001US-00966451.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NFAsppaB in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory diseases and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy
                                                                                                                                                                                                                                                                                                                                          Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC47549 standard; DNA; 31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 U; 0 Other;
                                                                                                                                                                                                             26-SEP-2002;
                                                                                                                                                                                                                                          10-APR-2003.
                                                                                                                                                                                                                                                                     WO2003028636-A2
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA complement sequence # SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
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                                                                                                                                                                                                              2002WO-US030574.
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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RESULT 14
AAS76803
ID AAS76
XX AAS76
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XX DNA e
XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sim:
Matches 156;
                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                     biodiversity.
                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                              WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The prophylaxis, or as research reagents or kits. The current sequence is utilised in an example from the invention in the design of antisense oligonucleotides, and represents the complement of the human DNA sequence that is given as GenBank accession number ACO16143
                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #12607.
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                                                                                                                                                                                                                                                                                                                                                                               HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGGT 13115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGA 182
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                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 1.7e-34;
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Claim 1; SEQ ID NO 12607; 103pp; English

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RESULT 15
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ID AAD400
XX AAD40
XX AAD40
XX Puman
XX Human
XX Human
XX Human
XX Infla
XX Inmun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) C sequences. (I) is useful as hybridiation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food cC supplement. (II) and its binding partners are useful in medical imaging CC situativity of (II). (I) and (II) are useful for treating disorders (IV) in abservant protein expression or biological activity. The CC diagnostice, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and to appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftb. wibo. int/bub/nublished sort segmences
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; death domain; DD; death effector domain; DED; Chlamydia infection; MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
                            17-NOV-2000;
29-JUN-2001;
                                                                                                                  15-NOV-2001; 2001WO-US044844.
                                                                                                                                                                                                                                            WO200240680-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IRAK4 short gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 TAAGGACATITGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTG
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                               2000US-00715893.
2001US-0301889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .180
                                                                                                                                                                                                                                                                                                  /product= "Human IRAK4 short protein"
                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC CC NIDD (NGPR-interacting Death Domain), with a candidate binding agent and CC detecting the association of the domain and the candidate binding agent, CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass CC spectroscopy (MS) and FPA. The invention is useful for modulating the CC level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell communoglobulin class switching, in particular apoptosis within a cell. CC muridarum, C: pneumoniae, and C. psittaci or a nucleic acid encoding the CC crostion is useful for detecting a Chlamydia infection. The CC complete is useful for detecting a Chlamydia infection. The CC complete is useful for detecting a Chlamydia infection. The CC contribody specifically caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of oncogenic proteins, CC discovery of drugs that suppress infection, inflammation, allergy, sepsis, substance of that suppress infection, inflammation, allergy, allergy, allegate, allergy arthritis, graft versus host diseases such as sepsis, fibrosis, CC arthritis, graft versus host disease. The invention is used in antisense CC therapy and gene therapy. The present sequence is human IRAK4 short gene XX
                                                                                                                                                                                                                                                                                                                                                               Matches 140; Conservative
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 211 BP; 77 A; 41 C; 36 G; 57 T; 0 U; 0 Other;
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SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS RESULT 1 AX431296 POCUS Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Sequence 5 from Patent WO0240680. AX431296.1 GI:21656165 DNA linear PAT 28-JUN-2002

ALIGNMENTS

REFERENCE AUTHORS JOURNAL HITLE Patent: WO 0240680-A 5 23-MAY-2002; BURNHAM INST (US) Pawlowski,K., Fiorentino,L., (Roth,W. and Stenner-Liewen,F. Novel death domain proteins Godzik, A., Lee, S.H., Reed, J.C.,

FEATURES source Location/Qualifiers

/codon_start=1/proteIn_id="CAD37274.1" /proteIn_id="CAD37274.1" /db_xref="GI:21656166" /translation="TYVRCINVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFH /translation="TYVRCINVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFH IRRFEALLQTGKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP" /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                            AX431306
Sequence 15 from Patent
AX431306
AX431306.1 GI:21656175
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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   Pawlowski,K.,
                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.
1 (bases 1 to 833)
Scanlan,M.J., Stockert,E., Chen,Y.-T., Old,L.J., Jager,E.
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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Sequence 10 from patent US 64
AR223870
                                                                                                                                                                                                                                                                    AATCAGTITCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                 ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                                                                                              ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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/mol_type="genomic |
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ative 0;
  Fiorentino, L.,
                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.8e-64;
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Godzik, A.,
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Lee,S.H.,
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Ś 망 Ś 밁 S 뮍 Ş В

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Matches 294;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. 1 (Dases 1 to 1636)
13. Chuang, T.H. and Ulevitch, R.J.

Human interleukin-1 receptor associated kinase 4 cDNA sequences
14. Unpublished
15. Chuang, T.H. and Ulevitch, R.J.
16. Chuang, T.H. and Ulevitch, R.J.
17. Direct Submission
18. Direct Submission
18. Submitted (14-JUL-2003) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Rd., La Jolla, CA 92037, USA
10561 Location/Qualifiers
1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1636 bp mRNA line Homo sapiens interleukin-1 receptor-associated mRNA, complete cds; alternatively spliced AY340962
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Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
BURNHAM INST (US)
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/db xref="G1:21656176"
/db xref="G1:21656176"
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SDTRFHSFSFYELKNVTNNFDERPISYGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLFGEDDLCLVYYMFMGSLLDRLSC
LDGTPPLSMHMFCKIAQGAANGINFLHENHHHHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEEIBDEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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mol_type="unassigned DNA"

db_xref="taxon:9606"
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Pred. No. 1.7e-64;
); Mismatches 0;
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Submitted (14-JUL-2003) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037, USA Location/Qualifiers
                                                    2 (bases 1 to 1684)
Chuang, T.H. and Ulevitch, R.J.
Direct Submission
                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini
1 (bases 1 to 1684)
Chuang, T.H. and Ulevitch, R.J.
Human interleukin-1 receptor associated
                                                                                                                                                                                                                                                                                                            AY340963 1684 bp mRNA linear PRI 01-AUG-
Homo sapiens interleukin-1 receptor-associated kinase 4 variant (IRAK4) mRNA, complete cds; alternatively spliced.
                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                         Unpublished
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                            AY340963.1 GI:37727960
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SDTRFHSFSFYELKNVTNNPDERPISVGNKNGEGFGVVYKGVNNTTVAVKLAAM
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LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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/codon_start=1
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Pred. No. 1.7e-64;
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                                                                                                                            kinase
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RESULT 6
CQ728380
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ACCESSION
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SOURCE
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                                        JOURNAL
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                   Patent: WO 02068579-A 14314 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                   Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a
                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                Sequence 14314 from Patent CQ728380 CQ728380.1 GI:42297030
                                                              thereof
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                               humanexons or transcripts,
                                                                                                                                                                                                                                                                                                                                   CQ728380
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Corporation (NY) (US)
Location/Qualifiers
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DDRYNGPHIRREBALLQTGKSPGTSELLEDWGTLWTVCDDLVDLLIQNEFFAPASLLLE
DAVPKTANTILENSKEAITYQOKOMFFCDKOFTLWTVCDDLVDLLIQNEFFAPASLLLEV
SDTRFHSFSFYELKNVTNNFDERFISVGGNKGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTELKQCPDQEIKVMAKCQHENLVELLGFSSDGDDLCLVVVYMPNGSLLDRLSC
LDGTPPLSWHRCKLAGAANGINFLHENHHIRDIKSANILLDBAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPFALRGEITPKSDIYSFGVULLEIITGLPAUDEHRE
ASEKFAQTVMTSRIVGTTAYMAPFALRGEITPKSDIYSFGVULLEIITGLPAUDEHRE
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QQLLQEMTAS"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAR02359.1"
/db_xref="GI:37727961"
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Pred. No. 1.7e-64;
; Mismatches 0;
                                                                               arrays, comprising for detecting expre
                                                                                                                                                                                                                                                                                                             75 bp DNA
WO02068579.
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DNA

linear

PAT

28-JUN-2002

Lee, S.H., Reed, J.C.,

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Query Match
Best Local Similarity
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Best Local Similarity
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                                                      254
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                                                                                                         194 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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Patent: US 6692959-A 3 17-FEB-2004;
Location/Qualifiers
1. .2817
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Bennett, C.F. and Freier, S.M.
Antisense modulation of IL-1 receptor-associated kinase-4
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Sequence 3 from patent US 6692959.
AR475548 1 GI:42715031
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                                              GAATTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                                              AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                        ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="genomic"
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                             100.0%; Score 294; DB 6; 100.0%; Pred. No. 1.6e-64; cive 0; Mismatches 0;
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AUTHORS
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DEFINITION
ACCESSION
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KEYWORDS
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Best Local Similarity
Matches 294; Conserv
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            Homo sapiens putative complete cds.
AF155118
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   AF155118.1
                                                           AF155118
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Sequence 27
AX431318
AX431318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pawlowski,K., Fiorentino,L., (Roth,W. and Stenner-Liewen,F. Novel death domain proteins Patent: WO 0240680-A 27 23-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                     ATCCAAAATGAATTTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                                                                                                              GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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ilarity 100.0%;
Conservative 0
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/db_xref="G1:21656188"
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VDITTEELKQQFDQEIKVMAKCQHENLVELLGFBDLCLVVYVMPNGSLLDRLSC
LDGTPFLSMHMGCKLAQAANGINFLHENHHIHRDIKSANIILLDBAFTAK1SDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEBIEDEKTIEDYIDKKMNDADSTSVEAMYSGASQCRHEKKNKSPDIKKV
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/mol_type="unassigned DNI
/db_xref="taxon:9606"
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                                           protein
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Pred. No. 1.6e-64;
); Mismatches 0;
                                                           2817
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WO0240680.
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se NY-REN-64 antigen mRNA,
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 7 AR475548

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AK000528 2820 bp mRNA line Homo sapiens cDNA FLJ20521 fis, clone KAT10395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigens recognized by autologous antibody in patients with renal-cell carcinoma
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                  AK000528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mikritestyvrclnvglirklsdfidpoggwkklavaikkpsg ddrynofhirreallotigksgtsellfdwgttnctvgdlvdllioneffarasllip davpktantleskealitotigksgtsellfdwgttnctvgdlvdllioneffarasllip davpktantleskealitvogokpecdbdrtlatevourlegskyrpsdssernkslev sdtrehefsptslknvtnnfdere is vggkwkegegfecvyykcyvnntyndyklam vditteelkoofdoeikvmakcohenlvellgfssdgddlclvyvympngslldrlscldtstplkgofdoeikvmakcohenlvellgfssdgddlclvyvympngslldrlscldtstpleskanginflenhhihrdiksanilldeaftakispeglar asekfaqtvmtsrivgtaymapealrgeitpeksdiysfgvchekknkspdikkvdhldikeeiedektiedyidkomdadstsveamysgasqcrhekknkspdikkvdhldldemtas"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 2817)
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/product="putative protein kinase NY-REN-64 antigen"
/protein ida="AAD42884.1"
/db_xref="GI:5360131"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
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Ota,T., Suzuki,Y., Obayashi,M., Ishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Ieogai,T. and Sugano,S.
NEDO human cDNA sequencing project
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                            GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                                                                                                                                                                                                             ACATATGTGCGCTCCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTGTGGATCTTTTTG
                                                                                              AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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ilarity 100.0%;
Conservative 0
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/db_xref="GI:7020684"

/db_xref="GI:7020684"

/translation="mankpitpstyurclinvglitrklsdpiddqggkklavaikkpsg

/translation="mankpitpstyurclinvglitrctvgdlutglitrgpasklillp

DAVPKYRANTILPSKEALITVQQKQMPFCDKDRTLMTPVQNLEQSYMPPDSSSPENKSLEV

SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAM

VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPHGSLLDRLSC

LDGTPPLSWHMRCKIAQAANGINLENHHIHEDIKSANILLDEAFTAKISDFGLAR

ASEKFAQTVMTSRIVGTTAYMARPALHGEITPKSDIYSFGVVLLEITTGLPAUDEHRE

PQLLLDIKEBIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV

QQLLQEMTAS"
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/cell_type="signet-ring cell carcinoma"
/clone_lib="KAT"
/note=_cloning vector pME18SFL3"
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mol_type="mRNA"

db_xref="taxon:9606"
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Pred. No. 1.6e-64;
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Submitted (25-APR-2003) Microbiology and Immunology, University
Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD
21201-1559, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N. Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
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Homo sapiens interleukin-1 recej
2 (IRAK4) mRNA, complete cds.
AY283671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medvedev, A.E., Lentschat, A., Kuhns, D.B., Blance, Salkowski, C., Zhang, S., Arditi, M., Gallin, J.I.
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                                          ACATATGTGCGCTGCATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTTATTGATCCT
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nilarity 99.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="IRAK-4 mutated form 2; truncated protein kinase due to frameshift and premature stop codon caused by deletion of positions 620-621 in the wild-type coding region" /codon_start=1
                                                                                                                                                                                                                           /gene="IRAK4"
/note="site of deletion mutation 2; as compared Accession Number AY283670 and wild-type IRAK4"
/replace="ac"
                                                                                                                                                                                                                                                                                           619^620
                                                                                                                                                                                                                                                                                                                                 /translation="mnkpitpstyvrclnvglirklsdfidpoegwkklavaikkpsg
Ddrynofhirrfeallotgksftsellfdwgtinctagdlvdllioneffapasllle
Davpktantlfskeaitvookomfcokdrtlwtpvonleosymppdssspenkslev
                                                                                                                                                                                                                                                                                                                     SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNNCGSEEACSNG
                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAP57090.1"
/db_xref="GI:31871820"
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="interleukin-1 receptor associated kinase 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IRAK4"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 4.3e-64;
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                                                  GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTTTG
                                                                                                                 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCCACTTCT
                               GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGCTGGTGATCTTGTGGATCTTTTG
                                                                                           AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                                     ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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Sequence 2 from Patent WO0151641.
AX196260
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                     /trainalation="makpitestyvrclnvglirklsdpidpoegwkklavaikkpsg
DDRYNQFHIRRFEALLQTGKSpTSELLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLP
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DAVPKTANTLPSKEAITVQQKQMEFCDKDRTLMTEVQNLEQSYMPEDSSSPENKSLENV
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VDITTEELKQVGPDQBEKVMAKCQHEBLUVELLGFSSDGDDLCLVFVYMRGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
                                                                                                                           PQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
QQLLQEMTAS"
                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/protein_id="CAC60090.1"
/db_xref="GI:15386463"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                          note="unnamed protein product; human IRAK-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="human IL-1 receptor-associated kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                     99.5%;
Score 292.4; DB 6
Pred. No. 4.3e-64;
0; Mismatches 1
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Best Local Similarity 99.7
Thes 293; Conservative
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Suzuki,N., Suzuki,S., Duncan,G.S., Millar,D.G., Wada,T.,
Mirtsos,C., Takada,H., Wakeham,A., Itie,A., Li,S., Penninger,J.M.,
Wesche,H., Ohashi,P.S., Mak,T.W. and Yeh,W.C.
severe impairment of interleukin-1 and Toll-like receptor
severe impairment of IRAK-4
Nature 416 (6882), 750-756 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (08-NOV-2001) Biology I,
South San Francisco, CA 94080, USA
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Homo sapiens interleukin-1 receptor associated kinase
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IRAK-4: a novel member
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                  ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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                                                                                                                                                                                                                                   /product="interleukin-1 receptor associated kinase 4"
/prote-in_id="AAM15772.1"
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/db_xref="GI:20219010"
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DDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLF
DAVPKTANTLESKEAITVQQKOMPFCDKDRTLMTPVQNLEQSYMPDDSSSPENKSLEV
SDTRFHSFSFYELKNVTNNFDKOMPFCDKMGEGFGVVYKGYVNNTVTAVEKKLAAM
VDITTEBELKQQFDQBIKVMAKCQHENLVELLGPSSDGDDLCLVYVYXMENGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKEAQTVMTSRIVGTTAYWAPEALAGEITPKSDLYSGGVVLLEIITGLPAVDEHRE
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QQLLQEMTAS"
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(mol_type="mRNA"
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                                                                                                                         Score 292.4; DB 9;
Pred. No. 4.3e-64;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1383)
                                                                                                                                                                                                                                          mutant form 1"
                                                                                                             LDGTPPLSWHMRCKIA"
                                                                                                                                                                                                                                                                                                                       gene="IRAK4"
                                                                                                                                                                                                                                                                                                                                                      gene="IRAK4"
                                                                                                                                                                                                                                                                                                                                                                                      'note="genotype:
                                                                                                                                                                                                                                                                                                                                                                 .1383
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Submitted (25-APR-2003) Microbiology and Immunology, Universit Marvland, Baltimore, 655 West Baltimore Street, Baltimore, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J. Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1383)
Medvedev,A.B., Lentschat,A., Kuhns,D.B., Blanco,J.C.G.,
Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
Bacterial Infections
J. Exp. Med. (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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1 (IRAK4) mRNA, complete cds.
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/note="site of mutation 1; replacement results in premature stop codon to glutamine amino acid change; compared to GenBank Accession Number AY283671 and wild-type IRAK4"
                                                                                                                                                                                                                                                              /protein_id="AAP57089.1"
/db_xref="qI:31871818"
/db_xref="qI:31871818"
/cranslat.on="makerIpsGtyVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
/cranslat.on="makerIpsGtyVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
DDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLP
DAVPKTANTLLPSKBAITVQQKQMFFCDKGTNATFVQNLEQGSYMPPDDSSSPENKSLEV
SDTREHSF8FYELKNVTNNTPDERF1SVGGNXWGEGGFGVVYKGYVNNTTVAVKKLAN
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"

/mol type="mRNA"

/mol type="mRNA"

/isolation source="patient hyporespsonsive to
lipopolysaccharide and interleukin-1 and suffering
lipopolysaccharide infections"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="IRAK-4 mutated form
to premature stop codon"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="interleukin-1 receptor associated kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9606"
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VERSION
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                                                                                                                                                                                                                                                                                                                Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                       Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC013316 1629 bp mRNA linear pr
Homo sapiens interleukin-1 receptor-associated kinase
clone MGC:13330 IMAGE:4287014), complete cds.
                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.3e-64;
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se 4, mRNA (cDNA
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 293;
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335
                                                                                                  275
                                                                                                                                                 181
                                                 241
                                                                                                                                                                                                                                                  121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 19 Row: n Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Rahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                            ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                  GAATTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGGGATCTTTTG
                                                                                                                                               GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                   ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                   AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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DDRYNQPHIREPALLQTGKSFTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLP
DAVFKTANTLSKEAITVQOKOMFOLKOT
DAVNQPHIREPAKLATVQOKOMFOLKOT
VONTTYPVQNLAGSTNYDELSE
SDTRFHSFSFYELKNVTNNFDERFISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEBLKQQFDQEIKVMAKÇQHENLVELLGFSSDGDDLCLVYVYMENGSLLDRLSC
LDGTFPLSWHMRCKIAQGAANGINFLHENHHIRDIKSANILLDEAFTAKISDFGLAR
LDGTFPLSWHMRCKIAQGAANGINFLHENHHIRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAFEALRGEITPKSDIYSGVVLLEIITGLJAVDEHRE
ASEKFAQTVMTSRIVGTTAYMAFEALRGEITPKSDIYSGAVGCLHEKKNKRPDIKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="IRAK4"
/codon_start=1.
/codon_start="interleukin-1 receptor-associated kinase
/protein_ida"AAH13316.1"
/db_xref="GI:15426432"
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/db_xref="LocusID:51135"
/db_xref="MIM:606883"
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/db_xref="MIM:606883"
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/clone_lib="NIH_MGC_56"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="MGC:13330 IMAGE:4287014"
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99.7%;
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Pred. No. 4.3e-64;
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Job time : 1848 secs

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Minimum |
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DB seq
A Geneseq_23Sep04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2001s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
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517
1 TYVRCLNVGLIRK
                                                                                                                                                                                                                                                                                                                                           2002273 seqs, 358729299 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            January 10, 2005, 23:07:39;
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231.286 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Aab65667 Novel pro		•	Ade28317 Human KPP	7 Human	Aae24864 Human IRA	Abg12616 Novel hum	Aae05406 Mouse IRA	Aae05405 Mouse IRA	Aae05399 Mouse int	Aae05404 Human IRA	Aae05403 Human IRA	Aae05401 Human IRA	Aae05398 Human int	Aae05402 Truncated	Ado44001 Amino aci	Abr44401 Human IL-	Aae38902 Human IRA	Aae38908 Human IRA	Aae24865 Human IRA	Human	Abg12618 Novel hum	Aay92347 Human can	Aae38897 Human IRA	Aae24854 Human IRA	Description	

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71	71.5	72	72.5	72.5	72.5	72.5	72.5	72.5	77	79	79	79	84	95	96.5	96.5	96.5	96.5	96.5
13.7	13.8	13.9	14.0	14.0	14.0	14.0	14.0	14.0	14.9	15.3	15.3	15.3	16.2	18.4	18.7	18.7	18.7	18.7	18.7
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ADF30722	ADK16042	ABB65115	ADP82021	ADN04325	AAU97838	ABP61489	AAB41026	AAU97836	AAE37948	AAY08654	ADE40441	AAY08653	ABG03007	ADB61346	ABG22715	AAM38644	AAB48172	ADI29275	AAB48173
	Adk16042 Streptomy	Abb65115 Drosophil	Adp82021 Human muc	Adn04325 Antipsori	Aau97838 Human cys	Abp61489 Human NF-	Human	Aau97836 Human cys	Murine	Aay08654 Human IRA	Ade40441 Human IRA	Aay08653 Human IRA	Abg03007 Novel hum	Adb61346 Murine IR	Abg22715 Novel hum	Aam38644 Human pol	Aab48172 Interleuk	Adi29275 Human MAR	Aab48173 Interleuk

ALIGNMENTS

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RESULT 1
AARZ4854
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23-MAY-2002.

(BURN-) BURNHAM INST

17-NOV-2000; 2000US-00715893. 29-JUN-2001; 2001US-0301889P. 15-NOV-2001; 2001WO-US044844.

Reed JC, Godzik A, Stenner-Liewen F; Pawlowski K, Fiorentino L, Lee SH, Roth W;

WPI; 2002-500222/53. N-PSDB; AAD40074.

New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.

Claim 1; Page 174; 209pp; English.

The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAPS, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent,

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RESULT 2
AAE38897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; allograft properties; infection; allograft properties; infection; allograft prostatic hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-l receptor-associated kinase; IRAK.
                                                                             (PAWL/)
(FIOR/)
                                                                                                                         (REED/)
(GODZ/)
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17-NOV-2000;
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) REED J C.
) GODZIK K.
) PAWLOWSKI K.
) FIORENTINO L.
) LEE S H.
) ROTH W.
) STENNER-LIEWEN !
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2000US-0367360P.
2001US-0301889P.
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ilarity 100.0%;
Conservative (
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Pred. No. 1.9e-60;
; Mismatches 0;
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Sequence

86

Å,

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The present invention provides novel death Domain (DD) and death effector CC domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis CC death domain containing protein Such as Chlamydia trachomatis CC death domain containing protein (NIDD) DD. The invention is useful for CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate CC binding agent and identifying an effective agent (e.g. protein or drug) that binds a DD, DED CC or NB-ARC domain with protein CC binding agent and identifying an effective agent (e.g. protein or drug) that binds the DD, DED or NB-ARC domain. The invention is also useful for CC condulating the level of cell process such as apoptosis, cell adhesion, CC cell proliferation, cell stress responses, responses to microbial CC infection and B cell immunoglobulin class switching. DDB, DED8 and NB-ARC domain and both cross are CC consists and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are CC inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, hyperplasia, keloid, benign prostatic hypertrophy, fibrosis, cfillammatory hyperplasia and smooth muscle cell proliferation in arteries of inflammatory hyperplasia and smooth muscle cell proliferation in arteries continuity balloon angloplasty (restenosis). The invention is also used in terleukin-1 receptor-associated kinase (IRAK)-4 DD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 34; 99pp; English.
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Stenner-Liewen
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iewen F;
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RESULT 3
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Best Local
                                                                          04-OCT-1999;
   05-OCT-1998;
                                                                                                                                                                                                                            WO200020587-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer associated antigen precursor from clone NY-REN-64.
                                                                                                                                                                                                                                                                                                                                                                              renal cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY92347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                              cancer associated antigen precursor; diagnosis; cytostatic
98US-00166300
                                                                          99WO-US022873.
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Pred. No. 1.9e-60;
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RESULT 4
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ABG112618
AC ABG11
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XX NOVe
XX NOVe
XX Huma
KW Huma
KW Hooc
XX Homc
OS Homc
XX Home
YX 11-C
XX 30-M
XX 31-M
PF 31-M
PR 23-A
XX Y
PR 31-M
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Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventing, diagnosing and/or treating disorders associated with abnormal expression of human cancer associated antigens.
                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
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  New isolated polynucleotide and encoded polypeptides, useful
                                                      WPI; 2001-639362/73.
N-PSDB; AAS76805.
                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #12609.
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                                                                                                                                                                                           HYSEQ INC.
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E, Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
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2000US-00649167.
                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Y, Old LJ,
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100.0%; P;
ative 0;
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Jager E,
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equences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used conditions are also used conditions are also used conditions. (II) is useful in gene therapy techniques to restore normal contivity of (II) or to treat disease states involving (II). (II) is converted to the say that the detecting or quantitating a converted in tissue, as molecular weight markers and as a food converted in tissue, as molecular weight markers and as a food converted in tissue, as molecular weight markers and as a food converted in tissue, as molecular weight markers and as a food converted in the supplement. (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The converted and polynucleotide sequences have applications in convertices, forensics, gene mapping, identification of mutations converted and to produce other types of data and products dependent on DNA and cand sequences of the invention. Note: The sequence data for this content did not appear in the printed specification, but was obtained in celectronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
Sequence
                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide sequences. (I) is useful as hybridisation probes.
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  455 AA;
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Matches
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                                                                     1 TYVRCLAVGLIRKLSDFIDÞQEGWKKLAVAIKKÞSGDDRYNQFHIRRFEALLQTGKSÞTS
                                                                                                           98;
                                                                                                                      Similarity
                   BLLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP 98
                                                     TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP 106
                                                                                                           Conservative
                                                                                                         100.0%; Score 517; DB 4; 100.0%; Pred. No. 1.5e-59; tive 0; Mismatches 0;
                                                                                                           Indels
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                                                                                                           Gaps
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Query Match

Length 455;

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RABSULT 5
AAB24 SA
AAB24 SA
AAB24 SA
AAB2 SA
AC AAB2
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Huma
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Human; death domain; DD; death effector domain; DED; Chlamydia infection NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsi inflammation; allergy; autoimmunity; allograft rejection; cell division immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy. Chlamydia infection; on; sepsis; division;

Human IRAK4 protein #1. 22-OCT-2002 (first entry)

WO200240680-A2

23-MAY-2002.

15-NOV-2001; 2001WO-US044844

17-NOV-2000; 29-JUN-2001; 2000US-00715893 2001US-0301889P

(BURN-) BURNHAM INST

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee E, Roth Ξ

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RESULT 6
AAE24865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC (CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and CC QU detecting the association of the domain and the candidate binding agent, CC CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent, CC QU detecting the association of the domain and the candidate binding agent, CC QU detecting the association of the domain and the candidate binding agent, CC QU detecting the association of the domain and the candidate binding agent, CC QU detecting the association of the domain and the candidate binding agent, CC QU detecting the suseful for medical cresonance (NMR), mass collaborate in the collaborate in particular apoptosis within a cell.

CC CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of concepts to treating bacterial infections by modulating the activity of bacterial proteins and artibody specific for it are useful for suseful for treating immune-based by the oncogenic proteins and for it useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, therease, the protein collaborate therapy and gene therapy. The present sequence is human IRAK4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                           Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease;
Homo sapiens
                                                                                                                                                                                                                                                                              Human IRAK4
                                                                                                                                                                                                                                                                                                                                                   22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                           AAE24865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE24865 standard; protein; 460
                                                                    lmmunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 183-184; 209pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYVRCLNVGLIRKLSDFIDÞÓEGWKKLAVAIKKÞSGDDRYNOFHIRRFEALLOTGKSÞTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AA;
                                                                                                                                                                                                                                                                           protein
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                                                         gene therapy; antisense therapy
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Pred. No. 1.6e-59;
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The invention relates to an isolated polypeptide comprising a death commain (DD), death effector domain (DED) or NB-ARC domain. The invention comprising a death commander of the comprising a binding agent, preferably a protein or a drug companied binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC commander of the domain and the candidate binding agent, DED4 or CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and companied companied commander of the domain and the candidate binding agent and companied companie
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 196-197; 209pp; English.
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29-JUN-2001; 2001US-0301889P
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460 AA;
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                                                                  AAE38908 standard; protein;
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                                                                                                                                                                      TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
                                                                                                                                                           TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALL
                                                                                                                     ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                              100.0%; Score 517; DB 5; 100.0%; Pred. No. 1.6e-59;
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WO200240680-A2

Human IRAK4 18-DEC-2003

protein

(first entry)

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CC domain (DED) proteins and nucleic acids encoding them. The invention also CC provides death domain containing protein such as Chlamydia trachomatis CC death domain containing protein (CTDD) DD and neural growth factor CC receptor-interacting death domain (NIDD) DD. The invention is useful for CC or NB-ARC domain from DAP3, IRAK4, (CTDD) DED4 or NIDD with a candidate CC binding agent and identifying an effective agent (e.g. protein or drug) that binds a DD, DED CC or NB-ARC domain from DAP3, IRAK4, (CTDD) DED4 or NIDD with a candidate CC binding agent and identifying an effective agent (e.g. protein or drug) CC that modulates the association of a DD, DED4 or NB-ARC domain with protein CC that binds the DD, DED or NB-ARC domain. The invention is also useful for CC domains the Level of cell process such as apoptosis, cell adhesion, CC cell proliferation, cell stress responses, responses to microbial CC domains and/or anti-DD5 anti-DED or anti-NB-ARC domain antibodies are CC useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allograft rejection, sepsis and other diseases. CD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte confilammatory hyperplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC converses and smooth muscle cell proliferation in arteries CC interleukin-1 receptor-associated kinase (IRAK)-4 protein
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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                                                                               Sequence 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides novel death Domain (DD) and death effector
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GODZIK A.
PAWLOWSKI K.
FIORENTINO L.
LEE S H.
                        Similarity
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    Conservative
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2000US-0367360P.
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    0;
                    Score 517; DB 5;
Pred. No. 1.6e-59;
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binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion,

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17-NOV-2000;
17-NOV-2000;
29-JUN-2001;
                                                   The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
                                                                                                                                                                                                                                                                                                        Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                        (REED/)
(GODZ/)
(PAWL/)
                                                                                                                                                                 Claim
                                                                                                                                                                                          New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                           Stenner-Liewen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE38902 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     keloid; interleukin-1 receptor-associated kinase; IRAK.
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FIORENTINO )
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jiewen F;
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9. .106
                                                                                                                                                                 99pp;
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Best Local
The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or
                                                                                                                                                                                                                                                                                                                                                                      kinase-4
treating
                                                                                                                                                                                                                                                                            Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-363256/34.
N-PSDB; ACC47548.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cance inflammatory disease; infection; diagnostic; therapeutic; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, heoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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Pred. No. 1.6e-59;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of human IRAK4.
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CC precursor, Pushover, a putative S-adenosylhomocysteinase, secretory CC carrier-associated membrane protein 2, surfeit locus protein 2, ubiquitin CC carboxyl terminal hydrolase 11, upstream regulatory element binding caphate caphar cross complementing protein 4 (isoform 1). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                              Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II,; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease; syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gut; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; II-1 receptor/Toll receptor; sarcoidosis; transgenic animal; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated from of human IRAK-4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE05402 standard; protein; 191 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP
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Pred. No. 1.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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68 60 0

13-JAN-2000; 2000US-0176395P 12-JAN-2001; 2001WO-US001171.

Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 protein.

24-SEP-2001 (first entry)

AAE05398 standard; protein; 460

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RESULT 12
AAE05398
ID AAE05
XX
AC AAE05
XX
AC AAE05
XX
DT 24-SE
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC disease syndrome (ARES), chronic obstructive pulmonary disease (e.g., altergic rhinitis), transplant rejection, autoimmune diseases (e.g., caritorial ripidises), cancer (e.g., solid tumours, skin cancer or lymphoma), corrected diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), corrected sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, corrected sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, corrected sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, corrected sepsis, inflammatory bowel disease (e.g., rash, contact dermatitis, atopic dermatitis), Behcet's syndrome, ankylosing spondylitis, gout, corrective colitis), Behcet's syndrome, ankylosing spondylitis, gout, corrective colitis), Behcet's syndrome, ankylosing spondylitis, gout, corrective colitis), Behcet's syndrome, ankylosing spondylitis, gout, crash-tripy or expression are used to inhibit taignal transduction crasulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor that activates which is used to inhibit signal transduction correct that activates which is useful for testing the function of IRAK-4 activity or expression are used to inhibit signal transduction of actor that activates which is useful for testing the function of CIRAK-4 activity or expression are useful for testing the function of Rakk-4 activations and for the cell. IRAK-4 is used to create a constructed by denerate models for the study of inflammatory constructed by deleting the residues after K191 in the wild type human constructed by deleting the residues after K191 in the wild type human constructed by deleting the residues after K191 in the wild type human constructed by deletin. Note: This sequence is not shown in the construction of the specification (AAE03398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK) -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory pulmonary diseases and diseases of the airway (e.g., adult respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 191 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 53; Page; 89pp; English.
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                                                                                                                                                                                                                                                                                          ELLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLPDAVP
                                                                                                                                                                                                                                                                                                                                                                                       TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 513; DB 4; Length 191; Pred. No. 1.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; theumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; Behcet's syndrome; antylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal.
Homo sapiens.
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Domain Domain /label= Death_domain
/note= "Also known as N-terminal
192. .460
/label= Central_kinase_domain Location/Qualifiers Central_kinase_domain domain"

WO200151641-A1

19-JUL-2001

12-JAN-2001; 2001WO-US001171

13-JAN-2000; 2000US-0176395P

(TULA-) TULARIK INC

Li S

2001-451860/48 AAD10197.

Novel human interleukin-1 receptor associated kinase polypeptide, for identifying modulators of the polypeptide for treating gout, allergic rhinitis, multiple sclerosis and skin cancer. asthma,

Fig 1; 89pp; English.

CC kinase (IRAK) -4 protection IRAK associate with activated II-1, II-18 and CC other receptors and act to transduce signals originating from the CC activated receptors, ultimately leading to a variety of downstream CC effects such as nuclear factor (NF)-kappas activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as CC pulmonary diseases and diseases of the airway (e.g., adult respiratory CC disease syndrome (ARDS), chronic obstructive pulmonary diseases (o.g., CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or CC allergic rhinitis), transplant rejection, autoimmune diseases (e.g., CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or CC diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 cordiated sepsis, onn-CD14 mediated sepsis, osteoarthritis, osteoporosis, CC dermatitis), diseases of the skin (e.g., rash, contact dermatitis, atopic CC dermatitis), Hencet's syndrome, anhylosing spondylitis, gout, CC sarcoidosis and ophthalmic diseases (e.g., crash, contact dermatitis, gout, CC contidosis and ophthalmic diseases (e.g., crash, contact dermatitis, gout, CC contidosis and ophthalmic disease (e.g., crash, contact dermatitis, gout, CC contidosis and ophthalmic disease (e.g., rash, contact dermatitis, gout, CC contidosis and ophthalmic disease (e.g., crash, contact dermatitis, gout, CC contidosis and ophthalmic disease and conditions. The inhibitors of CC contidosis and ophthalmic diseases and conditions of a transcorption of actor that activates on far interleukin-1 receptor (II-IR)/Toll conditions the activates on far activate on of a transcription of actor that activate and of a transcription of conditions and for the develorment of potential treatments of diseases and conditions and for the develorment of potential treatments. disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences The present sequence is human interleukin (IL)-1 receptor associated K)-4 protein. IRAK associate with activated IL-1, IL-18 as gene therapy and in ö

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE05401 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Pred.
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Homo sapiens. Synthetic.

Misc-difference Misc-difference 214 Location/Qualifiers 213 note= "Wild type Lys substituted with

/note= "Wild type Lys substituted with Ala"

WO200151641-A1

19-JUL-2001.

12-JAN-2001; 2001WO-US001171.

13-JAN-2000; 2000US-0176395P

(TULA-) TULARIK INC

Wesche H,

WPI; 2001-451860/48.

Novel human interleukin-1 receptor associated kinase polypeptide, for identifying modulators of the polypeptide for treating gout, allergic rhinitis, multiple sclerosis and skin cancer. asthma,

51; Page; 89pp; English.

The patent discloses interleukin (II)-1 receptor associated kinase (IF-4 proteins and their cDNAs. IRAK associate with activated II-1, II-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respirator) respiratory kinase (IRAK)

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ARESULT 14
AREO5403
ID AREO5
XX AREO5
XX AREO5
XX LITER Human
XX Human
XX Human
XX Human
XX Human
XX II; a
KW Chron
XX Chron
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II, antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple esclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylliis; II-1 receptor/Toll receptor; sarcoidosis; transgenic animal; mutant; mutein; variant; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences are also used in gene therapy and in antisense therapy. The present sequence is a mutant (K213A, K214A) of human IRAK-4 protein. Note: This sequence is not shown in the specification but is derived from human IRAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398)
                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE05403 standard; protein; 460 AA
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                                                                                                            WO200151641-A1
                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                             /note= "Wild type Ile substituted with Leu"
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99.0%;
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CC activated receptors, ultimately leading to a variety of downstream CC inhibitors are useful for treating inflammatory diseases such as nuclear factor (NF) kappaB activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as CC pulmonary diseases and diseases of the airway (e.g., adult respiratory CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or CC allergic rhinitis), transplant rejection, autoimune diseases (e.g., cradiovascular diseases (e.g., stroke and atherosclerosis), diseases of CC diabetes), cancer (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 (CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoprosis, CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, CC sardiovascular than activation are used to inhibit signal transduction CC resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll creeptor in a cell. They also inhibit the activation of a transcription CC resulting from the activate models for the study of inflammatory of inflammatory to generate models for the study of inflammatory of conhuman transgenic animal which is useful for testing the function of CC IRAK-4 in vivo, to generate models for the study of inflammatory of sequence is not shown in the specification but is derived from human CC animal transcription of this sequence is not shown in the specification but is derived from human CC TAK-4 (SEQ ID NO: 1) shown in figure 1 of the specification (AAE05398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses interleukin (IL)-1 receptor associated kinase (IRAK) -4 proteins and their cDNAs. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.
Sequence 460 AA;
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  Human IRAK-4 polymorphic variant (G17A).
                            24-SEP-2001
                                                                                AAE05404 standard; protein; 460
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                                                                                                                                                             61 ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP 98
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                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                  98.8%;
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                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                               Length 460
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19-JUL-2001.

Human; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; cardiovascular disease; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; alherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoprosis; psoriasis; dermatitis; sepsis; osteoarthritis; rash; osteoprosis; psoriasis; dermatitis; sepsis; osteoarthritis; rash; osteoprosis; psoriasis; dermatitis; sepsis; osteoarthritis; and osteoprosis; osteoarthritis; and osteoprosis; psoriasis; dermatitis; sepsis; osteoarthritis; and osteoprosis; osteoprosis; osteoarthritis; and osteoprosis; osteoprosis; osteoarthritis; and osteoprosis; osteoarthritis; osteoprosis; osteoarthritis; osteoprosis; osteoarthritis; osteoprosis; osteoarthritis; osteoprosis; osteoarthritis; osteoprosis; osteoarthritis; osteoprosis; osteoprosis; osteoarthritis; osteoprosis; osteoprosis; osteoarthritis Homo sapiens. Synthetic.

Misc-difference Location/Qualifiers

/note= "Wild type Gly substituted with Ala"

WO200151641-A1.

19-JUL-2001

12-JAN-2001; 2001WO-US001171.

13-JAN-2000; 2000US-0176395P

(TULA-) TULARIK INC

WPI; 2001-451860/48

Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.

Disclosure; Page; 89pp; English.

The patent discloses interleukin (II)-1 receptor associated kinase (IRAK) CC -4 proteins and their cDNAs. IRAK associate with activated II-1, II-18 CC and other receptors and act to transduce signals originating from the CC effects such as nuclear factor (NF) kappaB activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as nuclear factor (NF) kappaB activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as cCC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC quimonary diseases (e.g., solid tumours, skin cancer of the central nervous systemic lupus erythematosus, multiple sclerosis or cardiovascular diseases (e.g., solid tumours, skin cancer or lymphoma), CC disbetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC disbetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC disbetes), cancer (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic culcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout, CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and conditions and ophthalmic diseases and conditions. The inhibitors of conditions are ceptor in a cell. They also inhibit the activation of a transcription factor that activates NFkappaB in the cell. IRAK-4 is used to create a conditions and for the study of inflammatory diseases and conditions. The function of disease is not shown in the specification but is derived from human conditions is applicable variant (G17A) of human IRAK-4 protein. Note: This sequence is not shown in the specification but is derived from human conditions. Is shown in the specification of the specification of the specification (Amproxam) (Amproxam). the specification (AAE05398)

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밁 á 밁 S Matches Query Match Best Local 69 61 9 1 TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS 60 96; Similarity ELLFDWGTINCTVGDLVDLLIQNEFFAPASLLLPDAVP TYVRCLNVALIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS ELLFDWGTTNCTAGDLVDLLIQNEFFAPASILLPDAVP 106 Conservative 98.1%; 98.0%; 0 Score 507; DB 4; Pred. No. 3.4e-58; 0; Mismatches 2 98 Length 460; Indels 0 Gaps 83

Search completed: January 10, 2005, 23:21:49 Job time : 155 secs

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starch synthase DU
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N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
JQ1701	AC3025	F98259	F90877	D85842	G85816	A90899	G85718	F90854	A90769	D85741	G90968	E85631	A85693	G90996	T29584
hypothetical 33.2K	transcription requ	probable transcrip	probable host spec	probable tail fibe	hypothetical prote		tail	probable host spec	probable host spec	hypothetical prote	host specificity p	hypothetical prote	hypothetical prote	probable host spec	hypothetical prote

ALIGNMENTS

C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: D69877

uroporphyrin-III C-methyltransferase homolog ylnD -

Bacillus subtilis

RESULT D69877

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togaton, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K., A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Cinchi, M. Danchin, A. Baccession: D69877
A;Accession: D69877
A;Accession: D69877
                                                                                                                                                                               RESULT 2
A33170
                             tube protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 12-Apr-1991 #sequence revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37862; A33170
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C;Superfamily: Uroporphyrin-III C-methyltransferase
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Matches
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;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 GHYKKEEDF---EEKWKALATGI-----DTLVIYMGIKNVQQIERKLLENGRDGSTPAAF 195
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                                                                                                                                                                                                                                                                                                                                                              -DWGTTN-----CTYGDLVDLLIQNEFFAPASLLLPDAV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFE----ALLQTGKSPTSELLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
S.; Orth, K.; Wasserman, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
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Pred. No. 0.78
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 257;
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A;Molecule type: protein
A;Residues: 1-18,'X',20-21,'X',23-28,'X',30-38,'X',40-41,'X',43-45 <GOR>
C;Comment: This protein is synthesized in the liver and small intestine. The propeptide
C;Comment: This protein is a major component of the high density lipoproteins in plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA40749.1; PID:g202945 R;Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W. J. Biol. Chem. 257, 971-978, 1982 A;Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is A;Reference number: A05314; MUID:82098162; PMID:6798036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24700; S00298; A05314
R;Haddad, I.A.; Ozdovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, A;Reference number: A92558; MUID:87008540; PMID:3020028
A;Accession: A24700
                                                                                                                                                                                                                                                                                                                                                   A; Introns: 15/1; 66/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P04639; EMBL:J02597; NID:g202935; PIDN:AAA40745.1; R;Poncin, J.E.; Martial, J.A.; Gielen, J.E. Eur. J. Biochem. 140, 493-498, 1984
A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA. A;Reference number: S00298; MUID:84207987; PMID:6426956
A;Accession: S00298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-259 < PON>
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A; Residues: 1-259 < HAD>
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C;Species: Rattus norvegicus (Norway rat)
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A;Cross-references: FlyBase:FBgn0003882
C;Superfamily: Drosophila tube protein
                                                                                                                                                                                                    Superfamily: apolipoprotein A-I; Intestine; lipid binding; Keywords: cholesterol metabolism; HDL; Intestine; lipid binding; 11-18/Domain: signal sequence #status experimental <SIG>19-24/Domain: propeptide #status experimental <PRO>;25-259/Product: apolipoprotein A-I #status experimental <MAT>
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A;Molecule type: mRNA
A;Residues: 1-462 <LET>
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A;Title: Genetic and molecular characterization of tube, a Drosophila gene maternally
A;Reference number: A37862; MUID:91126085; PMID:1899484
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C;Genetics:
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                                                                                                                                    Matches
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Best Local
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                                                                   19 DPQEGWKKLA-----VAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCT
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                        EPQSQWDRVKDFATVYVDAVKDSGRDYVSQFESSTL----GKQLNLNLLDNWDTLGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |RKLSDFIDPQEGWKKLAVA|KKPSGDD-------RY----RY----NQFHIRR
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                                                                                                                                                   13.7%;
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                                                                                                                                                   Score 71;
Pred. No.
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                                                                                                                                                                    Length 259
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probable exported protein YPO2336 [imported] - Yersinia pestis (strain CO92) C;Bpccies: Yersinia pestis
C;Bpccies: Yersinia pestis
C;Bate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0284
R;Barkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.W.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davies, P; Dougan, G.; Il M.; Rutherford, K.; Simmonds, M.; Skelton, J; Stevens, K.; Whitehead, S.; Barrell, I Nature 413, S23-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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AI0284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: B64626
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.; A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily:
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A; Residues: 1-527 < TOM>
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997
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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 DDRYNOFHIRRFEALL---QTGKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLL
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                                                                                                                                                                                                       Similarity
                                    LVDLLIQNEFFAPASLLLPDAVP 98
                                                                              DFLIMDEQWKKIGIDGQKHSTENSFESFLMR--EKITQVDKSRMS-----TTN----
                                                                                                                        DFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTVGD
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Pred. No. 15;
11; Mismatches
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                                                                                                                                                                                                       Score 67;
Pred. No.
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                       9
                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                      Length 334
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C;Accession: C64714
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Autthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Aeference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64714
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision
hypothetical protein F8A5.28 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: B96633 C;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
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B96633
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asar
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada,
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Synechocystis sp. A; Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Synechocystis
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                                                                                                                                                                                                                                밁
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A; Residues: 1-299 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Croвв-references: UNIPROT:P55975; GB:AE000653; GB:AE000511; NID:g2314733; PIDN:AAD085
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Best Local
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                                                                                                                                                                                                                                                                            CTYGDLVDLLIQNEFFAPASL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENILVRKIAHLKAPSSHIINGYAHSNARVGVLIGIKYDNEKNAP
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                                                                                                                                                                                                                              GTVNDLLDQFVNQAFFADLAI 235
                                                                                                                                                                                                                                                                                                                             RRLADKLKERLGY--LGVYYKRKPS--HFYRNFSPQEKQEYLEDLSSQYREIILSYFSDE
                                                                                                                                                                                                                                                                                                                                                                            RKLSDFIDPQEGWKKLAVAIK-KPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTN
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     Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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28.4%; Pred. No. 9.8;
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ada, T.; Watanabe,
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da, M.; Yasuda
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     o
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     Alonso,
                       G-cadherin - sea urchin (Lytechinus variegatus)
c;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #
C;Accession: T30213
C;Accession: T30213
R;Miller, J.R.; McClay, D.R.
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McClay, D.R. 323-339, 1997

#text_change

09-Jul-2004

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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9US10; EME
A:Experimental source: strain 972h(-);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Zimmermann, W.; Wambutt, submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein SPAC607.08c [imported] - fission yeast (Schi C;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 C;Accession: T50228
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C; Genetics:
                                                                                                                                                                                                                                                                      A; Map position:
C; Superfamily: (
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                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-579 <ZIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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324
                                                                                     268 VTIGISGWLGDYNEVDAAWKSLTVGDKSYYWGDIYALKFEV---
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                                                                                                                                                                               28;
                                                                                                                               6 LNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYN-QFHIRRFEALLQTGKSPTSELLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
20; Conser
                                                                                                                                                                                                    Similarity
SAG-----LGWVKGEVISRTILAPLAAALWP 349
                                        DWGTTNCTVGDLVDLLIQNEFFAP-ASLLLP 94
                                                                                                                                                                                                                                                                      Caenorhabditis elegans hypothetical protein F35D11.3
                                                                                                                                                                          12.9%; Score 66.5; Ilarity 30.8%; Pred. No. 22; Conservative 13; Mismatches
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Library, December 1999
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Pred. No. 18;
15; Mismatches
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-); cosmid c607
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                                                                                                                                                                                                                       Length 579;
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                                                                                                                                                                               Indels
                                                                                          EALVDLGKS
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                                                                                                                                                                               11;
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Maiti, R.;
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Marziali,
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translation elongation factor EF-Ts - C;Species: Helicobacter pylori A;Variety: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: Strain 935c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asripson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm C.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E., F.G.; Nunes, L.R.; Oliveira, M.A.; M.S.; Marck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zancon annotation.
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                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aypothetical protein XF0172 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: A82839
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: XF0172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9PGX6; GB:AE003871; GB:AE003849; NID:g9104966; PIDN:AAF829
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                                                                                                                                                                  DYIVENSATSP 506
                                                                                                                                                                                                                 DLLIQNEFFAP 88
                                                                                                                                                                                                                                                         EGWGLYAESLGKELGLYQDAYNYF.
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Pred. No. 26;
B; Mismatches
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                                                   pylori
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C;Species: T
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A;Molecule type: DNA
A;Residues: 1-440 <KUR>
A;Residues: 1-440 <KUR>
A;Residues: 1-440 <KUR>
A;Cross-references: UNIPROT:(992V35; GB:AL591985; PIDN:CAC49284.1; PID:g15140770; GSPDB:GNA;Cross-references: UNIPROT:(992V35; GB:AL591985; PIDN:CAC49284.1; PID:g15140770; GSPDB:GNA;Cross-references: UNIPROT:(992V35; GB:AL591985; PIDN:CAC49284.1; PID:g15140770; GSPDB:GNA;Cactally Composite of the legume of the legume symbiont Sinchizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                      A;Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Proc. Natl. Acad. Sci. U.S.A. 98, 989-9994, 2001
A;Title: The complete sequence of the 1,883-kb pSymB megaplasmid from the N2-fixin A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95952
A;Status: preliminary
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R;Alm, R.A; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown,
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, (
Nature 397, 176-180, 1999
Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: D95952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable glycosyltransferase, forming alpha glycosyl linkages protein expE7
C;Species: Sinorhizobium meliloti
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A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
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;Genome: plasmid
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;Experimental source: strain J99
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                                           10 LIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 GENILVRKIAHLKAPSSHIINGYAHSNARVGVLIAIEYNNEKNAP 179
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Similarity
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                                                                                                                          12.6%;
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                                                                                                Score 65; DB
Pred. No. 23;
10; Mismatches
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Q.; Taylor, D.E.; Vovis, (
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aestivum

(common

wheat)

fructosyltransferase 2;

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C;Date: 18-Aug:2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Date: 18-Aug:2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: G82217 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 Nature 406, 477-483, 2000 Nature 406, 477-483, 2000 A;Title: DN Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: G82217
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A;Residues: 1-662 <KNA
A;Residues: 10-662 <KNA
A;Cross-references: UNIPROT:Q8W430; DDBJ:AB029888
C;Comment: This enzyme, which is a vacuole-type fructosyltransferase and a fructan-biosy
fers a fructosyl moiety from one sucrose to another, resulting in the formation of trisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004 C;Accession: JC7906 C;Accession: JC7906 R;Kawakami, A.; Yoshida, M. Biotechnol. Biotechnol. 66, 2297-2305, 2002 Biosci. Biotechnol. Biochem. 66, 2297-2305, 2002 A;Title: Molecular characterization of sucrose:sucrose 1-fructosyltransferase and sucrose A;Reference number: JC7905; MUID:22394650; PMID:12506964
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C;Keywords: glycosyltransferase; hexosyltransferase
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Search completed: January 10, 2005, 23:25:52 Job time : 41.secs
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C;Superfamily: 6-pyruvoyl tetrahydropterin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9KSF7; GB:AE004209; GB:AE003852; NID:g9655779; PIDN:AAF9445
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-122 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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                                                                                                                                   46 VDPHTGWVVDFAEIKAAFKPI-YDRLDHYYLNDIEGL----ENPTSEVLAKW 92
                                                                                                                                                                                              18 IDPOEGWKKLAVAIK---KPSGDDRYNOFHIRRFEALLQTGKSPTSELLFDW 66
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                                                                                                                                                                                                                                                         12.4%; Score 64; DB 2; Length 122; ilarity 34.6%; Pred. No. 6.3; Conservative 8; Mismatches 18; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 10, 2005, 23:08:19; Search time 193 Seconds
(without alignments)
292:159 Million cell updates/sec

Title:
Perfect score: 517
Sequence:
1 TYVRCLNVGLIRKLSDFIDP......LLIQNEFFAPASLLLPDAVP 98

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:
1825181

Minimum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:
UniProt_0:*
1: uniprot_sprot:*
2: uniprot_trembl:*
Pred. No. is the number of results predicted by chance to have a
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19.1 18.7 19.7 19.7 19.7 19.7 19.7 19.7 19.7 19	100.0 99.2 99.2 92.1 92.1 55.5	Query Match 1
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		BB
Q9CE40 Q9Y616 AAH57800 AAH69388 Q8X4B2 Q6X4B2 Q6Y1S1 AAO91937 Q7ZYE4 Q8C1XC0 Q9C1XC0 Q34744 Q9D1S0 Q8VC10 Q6PB60 AAH59871 MLT1_HUMAN TUBE_DROME Q8DMT6 Q8DMT	IRA4 HUMAN Q7Z6A7 Q7Z6A8 Q9D250 Q9D250 IRA4 MOUSE Q7ZVW7 Q6IWL3 AAT37635	ID
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	Interleukin-1 receptor-associated kinase-4 (EC	σ.	sequence update)	:ed)		PRT; 460 AA.				AT. T CHMENTS	AAS75798	Q6JEK7	Q7PMY3	AA024761	Q8CFA1	Q8CEA0	Q6YBS1	AA024762	Q8C5M0	Q6YBS0	Q88RV5	Q8CC82	Q6FSJ5	APA1_RAT
	(EC 2.7.1) (IRAK-4) (NY-				•						Aas75798 dasypus n	Q6jek7 dasypus nov	Q7pmy3 anopheles g	Aao24761 mus muscu	Q8cfa1 mus musculu	Q8cea0 mus musculu	Q6ybs1 mus musculu	Aao24762 mus muscu	Q8c5m0 mus musculu	Q6ybs0 mus musculu	Q88rv5 pseudomonas	Q8cc82 mus musculu	Q6fsj5 candida gla	P04639 rattus norv

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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschuls R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.R., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Raha Y.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Raha Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF445802; AAM15772.1; -.
EMBL; AF155118; AAD42884.1; -.
EMBL; AK000528; BAA91232.1; -.
EMBL; AY186092; AAM75440.1; -.
EMBL; BC013316; AAH13316.1; -.
HSSP; Q62838; 1LUF.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001245; Tyr Dkinase.
Pfam; PF00069; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
Prodom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; PALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; PALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; PALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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SUBUNIT: Interacts with TRAF6 and IRAKI.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. Pelle
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FUNCTION: Involved in ILIR-induced NF-kappa-B (NFkB)
well as the activation of mitogen-activated protein
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FDWGTTNCTVGDLVDLLIQNEFFAPASLLL£DAVP 	PQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS 	3; DB 2; . 1.6e-49 tches	hins D.B., Blanco J.C.G., Vogel S.N.; confer Hyporesponsivene kin-1 in a Patient wit ty; IEA. b42D2896DACBDFF9 CRC64	a; Vertebra dni; Homini		218 AA.	ELLFDWGTTNCTVGDLVDLLIQNEFFAFASLLLFDAVF 	EGWKKLAVAIKKPSGDDRYNQ GWKKLAVAIKKPSGDDRYNQ	517; DB No. 1.4e- atches	y similarity) y similarity) y similarity) acceptor (By acceptor (By AR_ 019354. VAR_ 019355. VAR_ 019356. (in Ref. 1). (in Ref. 2).
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A Zhang S., Arditi M., Gallin J.I., Vogel S.N.;

T "Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurre Bacterial Infections.";

Bacterial Infections.";

Bacterial Infections.";

Bacterial Infections.";

Bacterial Featons.";

R GO: GO:0005524; F:ATP binding; IEA.

GO: GO:0004872; F:protein kinase activity; IEA.

GO: GO:0004872; F:protein kinase activity; IEA.

GO: GO:0004872; F:receptor activity; IEA.

GO: GO:0004872; F:receptor activity; IEA.

GO: GO:0016740; F:transferase activity; IEA.

GO: GO:0004872; P:protein amino acid phosphorylation; IEA.

R GO: GO:0016740; P:transferase activity; IEA.

R GO: GO:0016740; P:transferase activity; IEA.

R GO: GO:0016740; F:transferase activity; IEA.

R GO: GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO: GO:0006979; P:protein amino acid phosphorylation; IEA.

R GO: GO:0006979; P:protein amino acid phosphorylation; IEA.

R FODOm; PD00001; Protein amino acid phosphorylation; IEA.

R ProDom; PD000001; Protein amino acid phosphorylation; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched
library, clone:9330209D03 product:interleukin-1 receptor-associated
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Diencephalon;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria;
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                               MEDLINE=21085660; PubMed=11217851; RIKEN FANTOM Consortium;
                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Diencephalon;
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     "Functional annotation
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E 292 AA
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                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32704 MW;
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of a full-length mouse cDNA collection.";
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 2.3e-49
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I
Sciurognathi; Muridae;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
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A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Okido T., Owa C., Saito H., Saito R., Sakai K.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,

A Okazaki Y., Sazuki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

A Muramatsu M., Hayashizaki Y.,

B Muramatsu M., Hayashizaki Y.,

B Muramatsu M., BAB32090.2; -.

B MGD; MGI:2182474; Irak4
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Diencephalon;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE-Diencephalon;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDN
prepare full-length cDNA libraries for rapid discovery of
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome k
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR011029; DEATH_like.
Pfam; PF00531; Death; 1.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016301; F:kinase activity; IBA, GO; GO:0004872; F:receptor activity; II GO; GO:0007165; P:signal transduction; InterPro; IPR000488; Death.
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STRAIN=C57BL/6J;
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[3]
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89
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                                        ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP
                                                                                                                                                    TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
ELLFDWGTTNCTVGDLVDLLVQIELFAPATLLLPDAVP
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6J; TISSUE=Diencephalon;
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                                                                                                                                                                                                                                                                                                                                                             21695 MW;
                                                                                                                                                                                                                                                                92.1%;
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                                                                                                                                                                                                                                                                   Score 476; DB 2;
Pred. No. 2.2e-45;
                                                                                                                                                                                                                                                                                                                                                             142B61EE8A614898 CRC64;
                                                                                                                                                                                                                                              Mismatches
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based on functional
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                                                                                                                                                                                                                                                                                               Length 197;
      106
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RESULT 5 IRA4_MOUSE

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RP SEQUENCE FROM N.A.

RC STRALN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Growse C.M., Schemer C.M., Schuler G.D., Malek N.K.,

RA Altschul S.F., Zeeberg B.B., Benaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Joquellano M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RX MEDLINE=22354683; PLUMPEd=12466851; DOI=10.1038/nature01266;
RA Nikaido I., Osato N., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchonni L., McKenzle L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petroysky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Avasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Verardo R., Wangher L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Vann Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Mayaski T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Mayashi A., Soshino M., Waterston R., Lander E.S., Rogers J.,
RA Hara A., Hashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=21957277; PubMed=11960013; DOI=10.1073/pnas.082100399;
Li S., Strelow A., Fontana E.J., Wesche H.;
"TRAK4: A novel member of the IRAK family with the properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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01-OCT-2004 (Rel. 45,
01-OCT-2004 (Rel. 45,
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Q8R4K2; Q80
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Rel. 45, Last annotation update)
receptor-associated kinase-4 (EC
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation
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Ciyosawa H.,
Gojobori T.,
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RESULT
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Best Local S
Matches 89
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932;
METHER STRAIN STRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF445803; AAM15773.1; -
EMBL; AK028837; BAC26146.1; -
EMBL; BC051676; AAH51676.1; -
HSSP; P36897; IIAS.
MGD; MGI:2182474; Irak4.
                                                                                                                                                     Eukaryota, Metazoa,
Actinopterygii, Neo
Cyprinidae, Danio.
                                                                                                                                                                                                                                                    Q7ZVW7 PRELIMINARY; PRT; 382 AA.
Q7ZVW7;
Q1_JUN-2003 (TrEMBLrel. 24, Created)
Q1_JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1_MAR-2004 (TrEMBLrel. 26, Last annotation updat
Similar to interleukin-1 receptor-associated kina
                                                                                                                              Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                         Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
BINDING
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                              Name=zgc:55553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; FALSE NEG. ATP-binding; Serine/threonine-protein kinase; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00531; Death; 1.
Pfam; PF00069; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of more than 15,000 ful and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).
-I- FUNCTION: Involved in IIIR-induced NF-kappa-B (NFkB) well as the activation of mitogen-activated protein pathways. Phosphorylates IRAKI (By similarity).
-I- SUBUNIT: Interacts with TRAF6 and IRAKI (By similarity).
-SUBUNIT: Belongs to the Ser/Thr protein kinase fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinf European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLFDAVP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000488; Death.
IPR000719; Prot_kinase.
IPR001245; Tyr_pkinase.
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                                                                                                                                                                           ) (Danio rerio).
; Craniata; Vert
Teleostei; Osta
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Pred. No. 6e-45;
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ATP (By similarity).
ATP (By similarity).
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                          Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                         Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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protein kinase family.
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d kinase
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AN HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
AN Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AN Exapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
AN Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AR Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AR Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AR Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
AN ARICHARD M.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
AN Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
AN Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AN Hiting M., Touchman J.W., Green E.D., Dickson M.C.,
AN Hiting M., Touchman J.W., Green E.D., Dickson M.C.,
AN Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Tones G. T. Marra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC045381; AAH45381.1; -.

R GO; GO:00045324; F:ATP binding; IEA.

GO; GO:0004672; F:Protein kinase activity; IEA.

R GO; GO:0004672; F:receptor activity; IEA.

R GO; GO:0004672; F:receptor activity; IEA.

R GO; GO:0007165; F:signal transduction; IEA.

R InterPro; IPR000488; Death.

R InterPro; IPR011009; BEATH like.

R InterPro; IPR011009; Kinase.

R InterPro; IPR011009; Kinase.

R InterPro; IPR000719; Prot_kinase.

R Pfam; PF000531; Death; 1.

R Pfam; PF00059; Pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

R ATP-binding; Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                             Q6IWL3 PRELIMINARY; PRT; 483 AA. Q6IWL3; CFCated) 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Interleukin-1 receptor-associated kinase 4.
SEQUENCE FROM N.A.
Phelan P.E. III, Mellon
Submitted (MAY-2004) to
                                                                                                             Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; '
Cyprinidae; Danio
                                                                                                                                                                           Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                  Name=irak4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S.J., Marra M.A.;
                                                                                      _TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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  M.T., Kim C.H.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                             ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 287; DB 2;
Pred. No. 1.1e-23
                                                                                                                                                                               (Danio rerio)
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RESULT 9
Q8C7U8
ID Q8C7
AC Q8C7

Q8C7U8;

PRELIMINARY;

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Best Local S
Matches 51
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001488; Death
InterPro; IPR011029; DEATH_like.
InterPro; IPR01109; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR0007290; Ser_thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Prodom; PD00001; Prot kinase; 2.

SMART; SM00220; STKC; 1.

SMART; SM00219; TYRC; 1.

SMART; SM00219; TYRC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS050011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Kinase; Receptor.

ATP-binding; Kinase; Receptor.

SEQUENCE 483 AA; 53708 MW; 5F0BDBAC250561F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Phelan P.B. III, Mellon M.T., Kim C.H.;
"Untitled.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniforma
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                            EMBL; AY616584; AAT37635.1; Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRAK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00531; Death; 1
Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-1 receptor-associated
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                                                                                                                                              TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS
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                                                                                                                                                                                                                                                                                                    483 AA;
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Pred. No. 1.4e-23;
9; Mismatches 25
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Pred. No. 1.4e-23;
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annotation update)
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RA Pukuda S., Puruno M., Hamagaki T., Arakawa T., Bono H., Carminci P., RA Hayashida K., Hayatsu N., Hamagaki T., Hara A., Hashizume W., RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., RM Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Harada A., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugaharak Y., Shibat Konno H., Okazaki Y., Muramatsu M., Hayatsiaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayatsiaki Reselected "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
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STRAIN=(57BL/6J;

The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDNAs.";
(Agrure 420:563-573(2002).")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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STRAIN=C57BL/6J;
MEDLINE=11085660; PubMed=11217851;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:C330013G03 product:similar to interleukin-l receptor-associated
kinase M, full insert sequence.
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Mammalia; Eutheria;
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Rodentia;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of new
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RESULT 10

QBCE4

JD QBCE4

AC QBCE4

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Best Local S
Matches 23
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GO; GO:0006468; P:protein amino acid
GO; GO:0007165; P:signal transduction
InterPro; IPR001029; DEATH like.
InterPro; IPR011029; Kinase like.
InterPro; IPR0100719; Prot kinase.
InterPro; IPR000719; Prot kinase.
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Q8CE40; Q8K1S8;
01-MAR-2003 (Tre
                                                                                                                                                        The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length CDNAs.",
Nature 420:563-573(2002).
                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Skin;
MEDLINE-2049374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Skin;
STRAIN=-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-OL-MAR-2003 (TrEMBLrel. 28, Last sequence update)
Ol-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732486H23 product:similar to interleukin-1 receptor-associated kinase M, full insert sequence (IL-1 receptor-associated
                   Carninci P., Shibata Y., Hayatsu N.,
Konno H., Okazaki Y., Muramatsu M.,
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                  RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated kinase M, kinase M).
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Pfam; PF00069; Pkinase; 1.
ProDom; PD0000001; Prot kinase; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM;
Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                             Nature
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STRAIN=C57BL/6J; TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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  subtraction
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Rodentia;
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Pred. No. 0.03
13; Mismatches
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cap-trapper-
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                                         Shibata K.,
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; Murinae; Mus
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annotation
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Q9Y616;
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                                                                                                             01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2004 (TrEMBLrel. 28,
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STRAIN=C57BL/6J; TISSUE=Skin;
                                                     IL-1 receptor-associated-kinase-M
kinase 3).
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EMBL; AJ440757; CAD29448.2; -.
MGD; MGI:1921164; Irak3.
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                                Name=IRAK3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22050158; PubMed=12054681; Rosati O., Martin M.U.;
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2 609 AA; 68455 MW;
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                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  (Human)
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                                                                                   (Interleukin-1 receptor-associated
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No. 0.036;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Hitalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Tonchman J.W., Green E.D., Dickeon M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                 Matches
                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                               ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
Kinase; Receptor.
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MEDILINE=99315891; PubMed=10383454;

Wesche H., Gao X., Li X., Kirschning C.J., Stark G.R., Cao Z.;

"IRAK-M is a novel member of the Pelle/interleukin-1 receptor-
associated kinase (IRAK) family.";
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC057880; AAH57800.1; -.
EMBL; BC069388; AAH69388.1; -.
Genew; HGNC:17020; IRAX3.
GO; GO:0004672; F:protein kinase activity; TAS.
GO; GO:0004702; F:receptor signaling protein serine/threonine..
GO; GO:0007166; F:cell surface receptor linked signal transdu...
GO; GO:0007166; P:protein amino acid phosphorylation; TAS.
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                          Pfam; PF00531; Death; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011099; Kinase like
InterPro; IPR000719; Prot_kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF113136; AAD40879.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                        ; Receptor.
CE 596 AA;
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                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
  TTNCTVGDLVDLL 80
                                                                         VGLIRKLSDFIDPOEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWG
                                      LGELCAVLDSCDGALGWRGLAERLSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SEP-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APR-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rescued clones,
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d clones, and Pla
PubMed=12477932;
                                                                                                                                                                                               67752 MW;
                                                                                                                                  18.7%;
                                                                                                                                                                                                                                                                                                                               Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ
                                                                                                                 12;
                                                                                                                 Pred. No. 0.05
2; Mismatches
                                                                                                                                    Score 96.5;
Pred. No. 0.
                                                                                                                                                                                          E37433EADD7E38BE CRC64;
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                                      -SWLDVRHIEKYVDQGKSGTRELLWSWA
                                                                                                                                                        BB
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                                                                                                                 31;
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                                                                                                                                                    Length
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                                                                                                               Gaps
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78

QKNKTIGDLLQVL

90

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AAH69388
ID AAH6
AC AAH6
AC AAH6
DT 20-W
DT 20-W
DT 10te
GN IRAH
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RX MEDLINE=22388557; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McEwan P.J., McKernan K.J., Makek J.A., Gunaratne P.H.,
RA Biskes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Rodriguez G. T. Mayra M. A.
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                                                                                                                                                                              RESULT 13
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Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Mammalia; Eutheria;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Interleukin-1 receptor-associated kinase 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057800; AAH57800.1; -.
                                                                    20-MAY-2004 (TrEMBLrel. 27, 20-MAY-2004 (TrEMBLrel. 27, 20-MAY-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase; Receptor.
SEQUENCE 596 AA;
                                                                                                                          AAH69388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissuE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                    Interleukin-1
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                    LGELCAVLDSCDGALGWRGLAERLSS-----SWLDVRHIEKYVDQGKSGTRELLWSWA 77
                                                                                                                                                                                                                                                                                                                                VGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWG 67
                                                                                                                                                                                                                                 QKNKTIGDLLQVL
                                                                                                                                                                                                                                                                    TTNCTVGDLVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Metazoa; Chordata; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                             PRELIMINARY;
                                                  TrEMBLrel. 27, Last sequence update)
TrEMBLrel. 27, Last annotation updat
receptor-associated kinase 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 67752 MW;
                                                                                                                                                                                                                                                                                                                                                                                           18.7%;
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Pred. No. 0.05
12; Mismatches
                                                                                                          Created)
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Schnerch A., Schein J.E.,
                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                31;
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       Euteleostomi;
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Q8K4B2

ID Q8K4B

AC Q8K4B

AC Q8K4B

DT 01-OC

DT 01-OC

DT 01-MA

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GN Name=

OC ELKAY

OC Mamma

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RA KODBA

RA KODBA

RA KODBA

RA KODBA

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RA KODBA

RA MEDLI

RA KODBA

RA MEDLI

RA GOBA

DR GO;

DR GO;
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RA Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
RA Altechul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Woczean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
RA Arnya M. A., Touch S., Schmutz J., Myers R.M., Schein J.E.,
RA Arnya S. 7. Mayra M. A.
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Best Local S
Matches 23
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01-OCT-2002
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                  Q8K4B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC069388; AAH69388.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                      Kobayashi K., Hernandez I.D., Ga
Medzhitov R., Flavell R.A.;
"IRAK-M is a negative regulator
Cell 110:191-202(2002).
                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                              Q8K4B2;
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EMBL; AF461763; AAM83393.1; -. MGD; MGI:1921164; Irak3. GO:0016301; F:kinase activity; GO; GO:0006468; P:protein amino aci
                                                                                                                                                 STRAIN=C57BL/6;
MEDLINE=22145925; PubMed=12150927;
                                                                                                                                                                                                                         NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                    Name=Irak3;
                                                                                                                                                                                                                                                                                                                      Interleukin-1 receptor-associated kinase
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 QXXXTIGDLLQVL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 LGELCAVLDSCDGALGWRGLAERLSS-----SWLDVRHIEKYVDQGKSGTRELLWSWA
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2 (TrEMBLrel. 22,
4 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                 Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 96.5; D
Pred. No. 0.05
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                 Galan J.E., Janeway C.A.
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                                                                                                  of Toll-like receptor signaling.";
       acid
                       IDA.
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   phosphorylation;
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Q6Y1S

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          밁
                                                                                                                                                                                                                                                                                                                                                                   C STRAIL-Wistar TISSUB=Spleen;
C STRAIL-Wistar TISSUB=Spleen;
A Li Y., Ji A., Schafer M.K.;
L Submitted (DBC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX191270; AA091937.1; -.
InterPro; IPR000488; Death.
InterPro; IPR010029; DBARH like.
InterPro; IPR000157; TIR.
IR InterPro; IPR000157; TIR.
IR Pfam; PF00531; Death; 1.
IR SMART; SM00005; DEATH; 1.
IR SMART; SM00005; DEATH; 1.
IR SMART; SM00255; TIR; 1.
IR SMART; SM00255; TIR; 1.
IR PROSITE; PS50017; DEATH_DOMAIN; 1.
IR PROSITE; PS50104; TIR; 1.
IR PROSITE; PS50104; TIR; 1.
IR PROSITE; PS50104; TIR; 1.
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Best Local S
Matches 28
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6Y1S1 PRELIMINARY; PRT; 296 AA.
Q6Y1S1;
Q6Y1S1;
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Myeloid differentiation primary response gene 88.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00531; Death; 1.
Pfam; PF00059; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Kinase; Receptor.
Kinase; Receptor.
SEQUENCE 609 AA; 68657 MW; 19E4D129F854DD73 CRC64;
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InterPro; IPR010488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR011009; Kinase like.
InterPro; IPR010719; Prot_kinase.
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Local Similarity 32.4%; Pred. No. 0.089;
hes 24; Conservative 12; Mismatches 28; Indels
67 GTTNCTVGDLVDLL 80
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77 AQKNKTIGDLLEVL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LIRKLSDFIDPQE---GWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDW 66
                                                                                                                                                                                                                                                            ch 17.0%; Score 88; DB 2; Length 296; I Similarity 35.0%; Pred. No. 0.23; 28; Conservative 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                   16;
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Search completed: January 10, 2005, 23:25:08 Job time : 195 secs

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq
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                                                                               of hits satisfying chosen parameters:
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length: 2000000000
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Match
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Maximum Match 100%
Listing first 45 summaries
         TYVRCLNVGLIRKLSDFIDP.....LLIQNEFFAPASLLLPDAVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length DB
         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
4 US-09-166-350-21
3 US-09-135-232-2
US-08-980-060-2
2 US-08-980-060-2
3 US-09-307-185-2
2 US-08-980-060-4
4 US-09-373-753-2
2 US-09-373-753-4
4 US-09-373-753-4
4 US-09-34-393-50
0 US-09-234-393-50
0 US-09-234-393-52
1 US-09-865-171-50
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0 US-09-865-171-52
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
62	62	62	62	62	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	63	63.5	63.5	63.5	64.5
12.0	12.0	12.0	12.0	12.0	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.2	12.3	12.3	12.3	12.5
428	428	428	428	428	1674	1674	1431	1423	680	520	499	125	430	501	501	501	662
4	4	4	w	ω	4	N	4	w	4.	4	4	4	4	4	w	N	4.
US-09-370-625A-7	US-09-557-800C-7	US-09-370-265-7	US-09-350-836B-7	US-09-608-285A-7	US-09-554-467A-12	US-08-968-542C-12	US-09-538-092-1198	US-08-810-712-10	US-09-248-796A-16453	US-09-724-623-124	US-09-543-681A-6427	US-09-543-681A-7171	US-09-489-039A-7580	US-09-773-753-6	US-09-307-185-6	US-08-980-060-6	US-09-534-228B-2
Sequence 7, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 1198, Ap	Sequence 10, Appl	Sequence 16453, A	Sequence 124, App	Sequence 6427, Ap	Sequence 7171, Ap	Sequence 7580, Ap	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli				

ALIGNMENTS

RESULT 1 US-09-166-350-21

GENERAL INFORMATION:

Sequence 21, Appl. Patent No. 644066

Application US/09166350A

APPLICANT: Scanlan, Matthew APPLICANT: Chen, Yao APPLICANT: Stockert, Elisabeth APPLICANT: Old, Lloyd APPLICANT: Jager, Elke APPLICANT: Knuth, Alex

Antigens

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-21
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Sequence 2, Application US/09135232
Patent NO. 6262228
GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/135,232
CURRENT FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 206
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/166,350A CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1998-10-05
UNMBER OF SEQ ID NOS: 35
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GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
INFORMATION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT FILING DATE: 1090-05-22
FRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
INMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
INFORMATION NUMBER: 09/135,232
FRIOR FILING DATE: 1998-08-17
INFORMATION OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
INFORMATION DATE: 1998-08-17
ORGANISM: human
US-09-863-549-2
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                                                                                                                                                                                                                                                              Patent No. 5965421
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Sequence
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Best Local Similarity
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Patent No. 6576444
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APPLICANT:
APPLICANT:
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ORGANISM: human
                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                             FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
COUNTRY: USA
ZIP: 20005-3934
MEDIUM TYPE: Floppy disk
                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600 CITY: WASHINGTON
                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                25 LGELCAVLDSCDGALGWRGLAERLSS-----SWLDVRHIEKYVDQGKSGTRELLWSWA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 VGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWG 67
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                                                                                                                                                                                                                                                                                                Application US/08980060
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DIXIT, VISHVA M.
                                                                                                                                                                                                                             NI, JIAN
FENG, PING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 96.5; DB 4; 31.5%; Pred. No. 0.00019; tive 12; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.7%; Score 96.5; I
31.5%; Pred. No. 0.00
tive 12; Mismatches
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Patent No.
INFORMATION FOR SEQ ID NO:
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                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/980
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEEPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
                                                                                                                                                                                                                         ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 36,688
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                               TELEPHONE:
                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UP
FILING DATE: Herewith
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 PIPAFPDSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 LRKIKSMERVOGVSITRELLWWWGMRQATVQQLVDLLCRLELYRAAQIILNWKPAPEIRC 101
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                                                                                                                                                                                                                                                                                                                                                    USA
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MUZIO, MARTA
DIXIT, VISHVA M.
            (202) 371-2600
(202) 371-2540
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                                                             1488.1010000/EKS/AJK
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RESULT 6
US-09-773-753-2
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Patent No. 6653452
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHANE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMGTH: 590 amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/980,060
FILING DATE: «UNKNOWN)
ATTORNEY/AGENT INFORMATION:
NAME: STEPPE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN IRAK-2 NUMBER OF SEQUENCES: 14
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                             45 IRRFEALLQT-GKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLL------
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42 LRKIKSMERVQGVSITRELLWWWGMRQATVQQLVDLLCRLELYRAAQIILNWKPAPEIRC 101
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amino acid
GY: linear
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                                                                         15.3%; Score 79; DB 4; Length 590; larity 31.9%; Pred. No. 0.051; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005-3934
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DIXIT, VISHVA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 79; DB 3; Length 590; 31.9%; Pred. No. 0.051; tive 12; Mismatches 19; Indels
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Sequence 4, Application US/09307185
Patent No. 6222019
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: PENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/980,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
             APPLICANT: PENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OP INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS
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Local Similarity 31.9%; Pred. No. 0.056;
Les 22; Conservative 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                   94 -----PDAV 97
                                                                                                                                                                                                                                                                                                                                         42 LRKIKSMERVQGVSITRELLWWWGMRQATVQQLVDLLCRLELYRAAQIILNWKPAPEIRC 101
                                                                                                                                                                                                                                                                                                                                                                  45 IRRFEALLQT-GKSPTSELLFDWGTTNCTVGDLVDLLIQNEFEAPASLLL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 625;
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Patent No. 6653452
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.3%; Score 79; DB 3; Length 625; Best Local Similarity 31.9%; Pred. No. 0.056; Matches 22; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein -09-307-185-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 CONTROL OF CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: STEFFE, ERIC K. REGISTRATION NUMBER:
                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NI, JIAN
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CLASSIFICATION:
            APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                   CITY: WASHINGTON
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SEQ ID NO 20
LENGTH: 398
TYPE: PRT
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
APPLICANT: Shillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: wsurl3885
                                                                                                                                                                                                                                                              Query Match
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Patent No. 6429014
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EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              Local Similarity
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,060
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                           167 VRRWDVSLVEGLPDFMKIAFEFWLKTSNELIAEAV-KAQGQDMAAYIRKNAWE-RYLEAY 224
284 LIELASRÍVDDA 295
                                 89 ----ASLLLPDA 96
                                                                                                         52 LQ-----FFAP----
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22; Conserv
                                                                   LQDAEWIATCHVPTFDEYLNNGTPNTGMCVL-NLIPLLLMGEHLPIDILEQIFLPSRFHH 283
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                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                      13.4%; Score 69.5; DB 31.1%; Pred. No. 0.62; ative 13; Mismatches
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                                                                                                                                                                                                                        Indels
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GENERAL INCOMP.

GENERAL INCOMP.

APPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

APPLICANT: Bohlman, Jorg

APPLICANT: Bohlman, Jorg

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRAN

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: WSUR113345

CURRENT APPLICATION NUMBER: US/09/234,393A

CURRENT APPLICATION NUMBER: 60/072,204

EARLIER APPLICATION NUMBER: 60/072,204

EARLIER APPLICATION NUMBER: 60/072,204

EARLIER APPLICATION NUMBER: 20

SEQ ID NO 24

LENGTH: 593

TYPE: PRT

ORGANISM: Abies grandis

US-09-234-393-24
                                                                                                                                             EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50
LENGTH: 593
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-234-393-50
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US-09-234-393-24
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Sequence 50, App...
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Best Local Similarity 31.1%;
Matches 41; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/234,393A CURRENT FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: WSUR113345
PRATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(817)
OTHER INFORMATION: Computer-generated protein sequence
                                                                          FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09234393A
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%; Pred. No. 1.1;
13; Mismatches
                                                                                                            of Artificial Sequence:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Bohlman, Jorg
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
TITLE OF INVENTION METHODS OF USE
FILE REFERENCE: WSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 593
RESULT 14
US-09-234-393-54
; Sequence 54, Application US/09234393A
; Patent No. 6265639
; GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Computer-generated protein sequence
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31.1%; Pred. No. 1.
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Crock, John E

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APPLICANT: Bohlman, Jorg

APPLICANT: Jetter, Reinhard

APPLICANT: Jetter, Reinhard

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: WSUR113345

CURRENT APPLICATION NUMBER: US/09/234,393A

CURRENT FILING DATE: 1999-01-20

EARLIER FILING DATE: 1998-01-22

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 54

LENGTH: 593

TYPE: PRT
                                                                                   ; SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 24
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-865-171-24
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Query Match 13.4%; Score 69.5; DI Best Local Similarity 31.1%; Pred. No. 1.1; Matches 41; Conservative 13; Mismatches
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LOCATION: (1)...(817)
OTHER INFORMATION: Computer-generated protein sequence
-09-234-393-54
                                                                                                                                                                                                                                                                  FILE REFERENCE: WSUR117468
CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/234,393
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/072,204
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SEGUITERPENE SYNTHASES
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-(NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Crock, John E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: protein
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Search completed: January 10, 2005, 23:26:36
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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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                   9 US-09-795-595-1

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14 US-10-001-254-26

9 US-09-863-549-2

15 US-10-405-114-54258

14 US-10-340-545-2

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9 US-09-773-753-2
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US-10-001-254-16
US-10-001-254-28
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Sequence 1, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 26, Appli
Sequence 2, Appli
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	-10-437-963-	-10-437-963-	10-437-963-142	82-122A	US-09-815-242-11374	-10-437-963-186	-10-437-963-1199	-10-041	893.	-09-900-797-5	09-903-0	US-09-887-586A-50	US-09-895-752-50	9-865-171-5	US-09-865-171-52	-09-865-171-5	71-	US-10-025-145A-20	US-10-316-253-289	US-10-316-253-287	US-10-316-253-285	US-10-316-253-277	09-987-107-2	0-378-083-		-10-024-	-217A-		10-024-298	-10-657-146	09-773-7	US-10-657-146-2
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ALIGNMENTS

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APPLICANT. Scenner-Liewen, Frank
APPLICANT. Scenner-Liewen, Frank
FILE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT EPELICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 60/715,893
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapien
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US-10-001-254-6
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Publication No. US20030049702A1
                                                                                          Query Match
Best Local 9
                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
                                                                                              Similarity
Roth, Wilfred
                                                                        100.0%; Score 517; DB 14; ilarity 100.0%; Pred. No. 4.5e-57; Conservative 0; Mismatches 0;
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US-10-001-254-28
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PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 28
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PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 16
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Best Local (
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                                                                                                                                                                                                                             APPLICANT: Roth, Wilfred APPLICANT: Stenner-Liewen, Frank TITLE OF INVENTION: No. US20030049702Alel Death Domain Proteins FILE REFERENCE: P-LJ 5037
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APPLICANT: Roth, Wilfred
APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT ETLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, APPLICANT: Godz
           LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT: Pawlowski, Krzysztof
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TYPE: PRT
ORGANISM: Homo sapien
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Roth, Wilfred
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Wo. US20030049702A1
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PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 460
TYPE: PRT
                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-595-1
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APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
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Best Local S
Matches 98
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Publication No. US20030059916A1
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APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT PEPLICATION UNMERS: US/09/795,595
CURRENT FILING DATE: 2001-01-11
                                                                                                                     LENGTH: 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.2%; Score 513; DB 9; Length 460; 99.0%; Pred. No. 1.1e-55; ative 0; Mismatches 1; Indels
  99.2%;
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Score 513; DB 10;
Pred. No. 1.1e-55;
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RESULT 6
US-09-795-595-3
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; ORGANISM: Mus sp.
US-09-795-595-3
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                                                                                                                  ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-759-595-3
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SEQ ID NO 3
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APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
TITLE OF INVENTION: UNBER: US/09/795,595
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
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                                        Matches
                                                                           Query Match
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APPLICANT: Li, Shyun
APPLICANT: Tilarik Inc.
APPLICANT: Tilarik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR PILING DATE: 2000-01-13
NUMBER OF 'SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                       Best Local Similarity
                                                                                                                                                                           LENGTH: 459
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                                        89; Conservative
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1 TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTS 60
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                                                         92.1%;
90.8%;
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Pred. No. 4.9e-51;
5; Mismatches 4
                                    Score 476; DB 10;
Pred. No. 4.9e-51;
5; Mismatches 4
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                                                                           DB 10;
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                                                                           Length 459;
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US-09-863-549-2
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TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1996-08-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapien
                                                                            Matches
                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09863549 Patent No. US20020049300A1
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Publication No. US200300497021
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PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: NO. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
CURRENT FILING DATE: 2001-11-15
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APPLICANT: Godzi
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                                                                                                                                                                          TYPE: PRT ORGANISM: human
                                                                                                                                                                                                            LENGTH: 596
                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Conservative
                                  8 VGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIRRFEALLQTGKSPTSELLFDWG 67
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                                                                                                Similarity
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LGELCAVLDSCDGALGWRGLAERLSS-----SWLDVRHIEKYVDQGKSGTRELLWSWA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFHIR
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Pawlowski, Krzysztof
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Roth, Wilfred
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                                                                                              18.7%;
31.5%;
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                                                                          Score 96.5; DB 9;
Pred. No. 0.0056;
2; Mismatches 31;
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                                                                                                              Length 596;
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                                                                                                                                                                                                ; LENGTH: 609
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-340-545-2
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10340545 Publication No. US20030157539A1 GENERAL INFORMATION:
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LENGTH: 644
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                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/340,545
CURRENT FILING DATE: 2003-01-09
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Flavell et al.
TITLE OF INVENTION: IRAK-M IS A NEGATIVE REGULATOR OF TOLL-LIKE RECEPTOR SIGNALING
FILE REFERENCE: YU-P01-011
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/348176 PRIOR FILING DATE: 2002-01-09
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 QKNKTIGDLLQVL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TINCTVGDLVDLL 80
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                                                       24
                     67
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                                                                                                                              24;
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GTTNCTVGDLVDLL 80
                                                   LLGELCGILDSWDGPLGWWGLAERLSN-----SWLDVRHIEKYLNQGKSGTRELLWSW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGELCAVLDSCDGALGWRGLAERLSS-----SWLDVRHIEKYVDQGKSGTRELLWSWA 125
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                                                                                                                              Conservative
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                                                                                                                                              18.4%;
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Pred. No. 0.0061;
2; Mismatches 31; Indels 7
                                                                                                                              Score 95; DB 14;
Pred. No. 0.0088;
2; Mismatches 2
                                                                                                                                                                 DB 14; Length 609;
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RESULT 12
US-09-773-753-2
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Patent No. US20020099177A1
GENERAL INFORMATION:
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APPLICANT: Powell, Douglas
APPLICANT: Wealch, Naddine S.
APPLICANT: Wealch, Naddine S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,
TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 12825, 9952, 5816,
TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-2.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 149
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION UNMBER: US/09/773,753
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
CLASSIFICATION: - Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,060
FILING DATE: - Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                    102 PIPAFPDSV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                    45 IRRFEALLQT-GKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLL------
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TYPE: amino acid
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ZIP: 20005-3934
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TELEFAX: (202) 371-2540
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STREET: 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 79; DB 9; Length 590; ilarity 31.9%; Pred. No. 0.89; Conservative 12; Mismatches 19; Indels
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DIXIT, VISHVA M.
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E, N.W., SUITE 600
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RESULT 14
US-10-657-146-2
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; ORGANISM: Homo Sapien
US-10-366-288-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10657146 Publication No. US20040110926A1 GENERAL INFORMATION:
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Best Local
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PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380,249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/366,288
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                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/657,146
FILING DATE: 09-5ep-2003
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US/08/980,060
FILING DATB: Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/391,306 FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/417,508 FILING DATE: 2002-10-10
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                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                         CITATE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600 CITY: WASHINGTON
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                           20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUZIO, MARTA
DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JIAN
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31.9%;
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Pred. No. 0.89;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-773-753-4
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US-09-773-753-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09773753
Patent No. US20020099177A1
GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                TELEFAX: (202) 371-: INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/980,060 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARB: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN IRAK-2 NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 PIPAFPDSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 -----PDAV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 LRKIKSMERVQGVSITRELLWWWGMRQATVQQLVDLLCRLELYRAAQIILNWKPAPEIRC 101
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22; Conserv
                                                                                                                                                                                                                                                      NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/773,753 FILING DATE: 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 590 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE: STERNE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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DIXIT, VISHVA M.
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202) 371-2540
                                                                                                                                                                                                                      (202)
15.3%;
31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                    <Unknown>
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Pred. No. 0.89;
2; Mismatches
Score 79; DB 9;
Pred. No. 0.96;
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                 Length 625;
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Matches	22;	22; Conservative	12;	12; Mismatches 19; Indels 16; Gaps	19;	Indels	16;	Gaps	2;	
Ş	45 IF	45 IRRFEALLQT-GKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLL 93	SELLED	WGTTNCTVGDLV	DLLION	EFFAPASLI	L		93	
οь	42 LF	12 LRKIKSMERVQGVSITRELLWWWGMRQATVQQLVDLLCRLELYRAAQIILNWKPAPEIRC 101	RELLWW	WGMRQATVQQLV	DLLCRL	ELYRAAQII	LINWKP	APEIRC	101	
8	94	94PDAV 97								
DЬ	102 PJ	102 PIPAFPDSV 110								
Search completed: J. Job time : 146 secs	mpleted	Search completed: January 10, 2005, 23:37:31 Job time : 146 secs	2005,	23:37:31					-	

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -Q=(cgn2 1)USPTO spool h /US1000154/runat 10012005 172741 10536/app query.fasta_1.263
-Q=(cgn2 1)USPTO spool h /US1000154/runat 10012005 172741 10536/app query.fasta_1.263
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=hunan40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10001254 @CGN 1 480 @runat 10012005 172741 10536
-NCFU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -MAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDE10 -XGAPEXT=0.5
-FGAPDP=6 -FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Command line parameters:
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517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4300275 seqs, 2872944193 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
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/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq: *
/ cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Ggn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _6/ptodata/1/pubpna/US07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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1210.961 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	No. 1 NO. 1 NO	1
	SCORE 5100 Te	
	100.00 10	}
	Length	
	DB 144 114 116 116 116 116 116 116 116 116	
ALIGNMENTS	1D 10 10 10 10 10 10 10 10 10	
	Sequence 15, Appli sequence 2, Appli sequence 3, Appli sequence 4, Appli sequence 4, Appli sequence 10, Appli sequence 4, Appli sequence 10, Appli sequence 10, Appli sequence 10, Appli sequence 10, Appli sequence 26096, Appli sequence 26096, Appli sequence 1, Appli sequence 14, Appli sequence 14, Appli sequence 14, Appli sequence 14, Appli sequence 3589, Appsequence 3589, Appsequence 3587, Appsequence 3589, Appsequence 358	

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GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

APPLICANT: Godzik, Krzysztof

APPLICANT: Howlowski, Krzysztof

APPLICANT: Piorentino, Loredana

APPLICANT: Lee, Sug Hyung

APPLICANT: Lee, Sug Hyung

APPLICANT: Stenner-Liewen, Frank

TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins

TITLE REFERENCE: P-LJ 5037

CURRENT APPLICATION NUMBER: US/10/001,254

CURRENT APPLICATION NUMBER: 60/301,889

PRIOR APPLICATION NUMBER: 60/301,889

PRIOR APPLICATION NUMBER: 09715,893

PRIOR APPLICATION NUMBER: 09715,893

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 62
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Sequence 5, Application US/10001254 Publication No. US20030049702A1

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; TENGTH: 1383
; TYPE: DNA
; ORGANISM: HOMO 8A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(
US-10-001-254-15
    Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-10-001-254-15
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-001-254-6 (1-98) x US-10-001-254-5 (1-294)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(294)
US-10-001-254-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ
SEQ ID NO 5
LENGTH: 294
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APPLICANT: Godzi
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ORGANISM: Homo sapien
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Roth, Wilfred
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Fiorentino, Loredana
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No. US20030049702A1
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Matches:
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Best Local Similarity:
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Query Match:
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CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
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Publication No. US20030087856A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freter
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS)
FILE REFERENCE: RTS-0324
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (50)...(1432)
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GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                  AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                       AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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Conservative:
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254 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG

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APPLICANT: Roth, Wilfred
APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: NO. US20030049702A1el De:
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
FOURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER: OF SEC ID NOS: 62
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Sequence 3, Application US/10630399
Publication No. US20040019009A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
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LENGTH: 2817
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Publication No.
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APPLICANT: Godz
APPLICANT: Pawl
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NAME/KEY: CDS
LOCATION: (50)
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      IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

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Lee, Sug Hyung
Roth, Wilfred
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Wo. US20030049702A1
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APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Me
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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US-09-795-595-2
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (1)..(1383)
OTHER INFORMATION: human IRAK-4
                                                                  OTHER INFORMATION: human OTHER INFORMATION: cDNA
                                                                                                                                                           TYPE: DNA
                                                                                                                                 ORGANISM: Homo sapiens
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LOCATION: (50)...(1432)
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                                                                                                               FEATURE:
                                                                                                                                                                               LENGTH: 1383
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                                                                                        receptor-associated kinase 4 (IRAK-4)
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Sequence 2, Application US/0975955
; Sequence 2, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
   APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; CURRENT APPLICATION NUMBER: US/09/759,595
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTMARE: Patentin Ver. 2.1
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Best Local Similarity:
Query Match:
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                                               US-10-001-254-6 (1-98) x US-09-759-595-2 (1-1383)
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US-09-759-595-2
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                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
                                                                                                                                                                                                              LOCATION: (1)..(13
OTHER INFORMATION:
                                                                                                                                                                                                                                                                        OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                               ENGTH: 1383
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ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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; OTHER INFORMATION: murine IL-1 r
; OTHER INFORMATION: cDNA
; NAME/KEY: CDS
; LOCATION: (163)..(1542)
; OTHER INFORMATION: murine IRAK-4
US-09-795-595-4
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DB:
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Best Local Similarity:
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US-09-795-595-4
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APPLICANT: Wesche, Holger
APPLICANT: Wesche, Holger
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/795,595
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro
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Sequence 4, Application US/09759595

| Sequence 4, Application US/09759595
| Publication No. US20030059916A1
| GENERAL INFORMATION: USANTION: Papelicant: Wesche, Holger
| APPLICANT: Tularik Inc.
| APPLICANT: Tularik Inc.
| APPLICANT: Tularik Inc.
| TITLE OF INVENTION: IRAK-4: Compositions and Methods of FILE REFERENCE: 018781-003910US
| CURRENT APPLICATION NUMBER: US/09/759,595
| CURRENT FILING DATE: 2001-01-13
| PRIOR APPLICATION NUMBER: US 60/176,395
| PRIOR APPLICATION NUMBER: US 60/176,395
| PRIOR APPLICATION NUMBER: US 60/176,395
| PRIOR PRIOR FILING DATE: 2000-01-13
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 4
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                                                                                                         GENERAL INFORMATION:
                                                                                                                        Sequence 149, Application US/09833790 Patent No. US20020068288A1
APPLICANT:
APPLICANT:
APPLICANT:
           APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
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LOCATION: (163)..(1542)
OTHER INFORMATION: muri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
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Percent Similarity:
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; OTHER INFORMATION: n = A,T,C
US-09-833-790-149
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                                                                    Score:
                                                                                       Pred. No.:
                                                                                                   Alignment Scores:
                                                                                                                                      US-09-966-451-10
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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 501
                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09966451 Publication No. US20030087856A1 GRNERAL INFORMATION:
                                                                                                                                                                                                                        SEQ ID NO 10
                                                                                                                                                                                                                             APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
ITILE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
                                                                                                                                                                    ORGANISM: Homo
                                                                                                                                                                                     LENGTH: 31000
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(501)
                                                                                                                                                      FEATURE:
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Sequence 25, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
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Best Local Similarity:
Query Match:
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US-10-630-399-10
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Pred. No.:
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LENGTH: 31000
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APPLICANT: Susan M. Freter
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/10/630,399
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: US/9/966,451
PRIOR PILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
              APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: NO. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
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ORGANISM: Homo sapiens
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Sequence 26096, Application US/10242535A
; Sequence 26096, Application No. US20040013663A1
; Dublication No. US20040013663A1
; GENERAL INFORMATION:
   APPLICANT: Chondrogene Inc.
; APPLICANT: Liew, C.C.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR RILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 211
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
FEATURE:
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; LOCATION: (1)...(177)
US-10-001-254-25
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Query Match:
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                                                                                            Pred. No.:
                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                        LENGTH: 470
TYPE: DNA
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                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 26096, Application US/10085783A

Publication No. US20040037841A1

REPLICANT: Chondrodene Inc.

APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

ITILE OF INVENTION: COMPOSITIONS and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT APPLICATION NUMBER: US/10/085,783A

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,917

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOPTWARE: PATEENTIN VERSION 3.2

SEQ ID NO 26096

LENGTH: 470

TYPE: DNA

ORGANISM: Human

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US-10-085-783A-26096
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Search completed: January 12, 2005, 09:54:48 Job time : 478 secs
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                                                                                                                                                                                                                                       139 ACATATGTGCGCTGCATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AsnGlnPheHisIleArg 46
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259 AATCAGTTTCACATAAGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 198
                                                                               259 AATCAGTTTCACATAAGA 276
                                                                                                    41 AsnGlnPheHisIleArg 46
                                                                                                                                                                                   21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspAspArgTyr 40
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Result
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-Q=/cgn2_1/USPTO_spool h/US10001254/runat_10012005_172738_10451/app_query.fasta_1.263
-Q=/cgn2_1/USPTO_spool h/US10001254/runat_10012005_172738_10451/app_query.fasta_1.263
-DB=N Geneseq_325ep04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-DB=N Geneseq_325ep04 -QFMT=fastap -SUB=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=20 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-LOCAL -OUTFMT=pco -NORM=sect -HEARSIZE=500 -MINLENS=0 -MAXLEN-200000000
-USER-US10001254 @CGN 1 1 470 @runat 10012005_172738_10451 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAXIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN ITHEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -MARN ITHEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                         Score
    517
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3: geneseqn2000s:*
4: geneseqn2001as:*
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Match
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Ygapop 10.0,
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Delop 6.0,
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first 45 summaries
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AAD59061
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Aad40074 Human IRA
Aad59056 Human IRA
Aaa09319 Human Can
Aad40079 Human IRA
Aad59061 Human IRA
Aa876805 DNA encod
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Abk73720 Bacillus		4.	14.4	74.5	44
Abk53369 Human eos	6 ABK53369	N	14.4	74.5	43
Adm02024 Human cDN	L1 ADM02024		4.6	75.5	42
Aad57286 Murine My	Þ	თ		77	41
0	N	864]	5	78.5	40
Adj30963 Human mus			5	•	39
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Abx60213 cDNA enco			5	•	37
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			6.2	84	28
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			8.7	96.5	24
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Adi29393 Human MAR			8.7	•	22
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uman	6 ABQ56733		6.0	134.5	20
9		2432	7.8	247	19
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DNA er			7.8	247	17
Human			7.8	247	16
T.	AAD40084		œ	247	15
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Aad59067 Human IRA	AAD590	æ	00.0	517	œ
Aad40085 Human IRA	AAD4008	17	100.0	517	7

ALIGNMENTS

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RESULT 1
 Human; death domain; DD; death errector uomain; pur, commission; sepsis; MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                             Human IRAK4 DD (death domain) cDNA.
                                                                                                                                                                                                                                                                                                               AAD40074;
                                                                                                                                                                                                                                                                                                                                       AAD40074 standard; cDNA; 294
15-NOV-2001; 2001WO-US044844.
                        23-MAY-2002.
                                                 WO200240680-A2.
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                       22-OCT-2002
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                    Location/Qualifiers
                                                                                   product= "Human IRAK4 DD"
note= "No start and stop codon"
                                                                        'partial
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                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent, and detecting the association of the domain and the candidate binding agent, compared two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell evel of a cell process such as cell proliferation and B cell communoglobulin class switching, in particular apoptosis within a cell immunoglobulin class switching, in particular apoptosis within a cell cantibody specifically reactive with CTDD DD C. trachomatis, C. CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The convention is useful for modulating the activity of oncogenic proteins, treating a pathology caused by the oncogenic proteins and for treating a pathology caused by the oncogenic proteins and for corteins by modulating the activity of bacterial for corteins by modulating the activity of bacterial for sepsis, altermanity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, thorease, therefore the activity of bacterial protein and gene therapy. The present sequence is human IRAK4 DD cDNA
                                                                                                                                                                                                                                                                                                                                                                       Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                No:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
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29-JUN-2001; 2001US-0301889P
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                         GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                                                               AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                    GlnGluGlyTrpLysLysLeuAlaValAlaIIleLysLysProSerGlyAspAspAspArgTyr
GAATTACTGTTTGACTGGGGGCACCACAAATTGCACAGTTGGTGATCTTTGTGGATCTTTTG 240
                                                                                                                                                                                                                            ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                            ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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iewen F;
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RESULT 2
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XX Huma
XW Huma
XW Chlla
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The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD and neural growth factor identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
17-NOV-2000;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation,
                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 33-34; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; death Domain; DD; death effector domain; DED; cell proliferation; Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; inflammation; allograft rejection; CTDD; cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-l receptor-associated kinase; IRAK; gene; ss.
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(GODZ/)
(PAWL/)
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DB; AAE38897.
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GODZIK A.
PAWLOWSKI K
FIORENTINO
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2000US-0367360P.
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/product= "Human IRAK4 DD protein"
/note= "No start and stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human interleukin-1 receptor-associated kinase (IRAK)-4 DD cDNA
                                                                                                                                                                                                                                                                                                                               AAA09319 standard; DNA; 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 294 BP; 84 A; 55 C;
            05-OCT-1998;
05-OCT-1998;
                                                  04-OCT-1999;
                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTACT
                                                                                                                                                                                                                                                 associated antigen precursor DNA, clone NY-REN-64
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                          cancer
            98US-00166300
98US-00166350
                                                  99WO-US022873.
                                                                                                                                          Location/Qualifiers 50. .670
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                           Human; death domain; DD; death effector domain; DED; Chlamydia infection; MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
                                                                                                                  Human IRAK4 gene
                                                                                                                                                                                                       AAD40079
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P-PSDB; AAY92347.
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                         immunosuppressive; gene therapy; antisense therapy; gene;
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E, Chen Y,
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Homo sapiens

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Best Local Similarity:
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                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention consists useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain in the candidate binding agent and controlled the association of the domain and the candidate binding agent and detecting the association of the domain and the candidate binding agent and controlled the 
                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                   Sequence 1383 BP;
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29-JUN-2001; 2001US-0301889P.
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                        ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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    The present domain (DED)
                                                       New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                     Claim 19; Fig 10A; 99pp;
                                                                                                                                            Stenner-Liewen F;
                                                                                                                                                          Reed JC,
                                                                                                                                                                                                                                         (REED/)
(GODZ/)
                                                                                                                                                                                                                                                                           29-JUN-2001;
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17-NOV-2000;
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                                                                                                                                                                                          FIORENTINO
LEE S H.
ROTH W.
                                                                                                                                                                                                                          REED J C.
GODZIK A.
PAWLOWSKI K.
                                                                                                                                                                                STENNER-LIEWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-1 receptor-associated kinase;
                                                                                                                                                       Godzik A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention provides novel death Domain (DD) proteins and nucleic acids encoding them.
                                                                                                                                                                                                                                                                         2000US-00715893.
2000US-0367360P.
2001US-0301889P.
                                                                                                                                                                                                                                                                                                                        2001US-00001254
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                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1383
                                                                                                                                                                                                                                                                                                                                                                                        /product= "Human IRAK4 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA; 1383
                                                                                                                                                         Pawlowski
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                                     English.
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                                                                                                                                                       Lee
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                                                                                                                                                      Roth W;
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                                                                                                                                                                                                                                                                                 AAS76805 standard; cDNA; 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1383
                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                         DNA encoding
                                                                                                                                                                                                                13-FEB-2002
                  11-OCT-2001
                                                    WO200175067-A2
                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                        GAATTACTGTTTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel human diagnostic protein #12609
                                                                                                                                                                                                              (first entry)
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517.00
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Matches:
Conservative:
Mismatches:
Indels:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) consequences. (I) is useful as hybridisation probes, polymerase chain consequences. (I) is useful as hybridisation probes, polymerase chain consequence (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consequences. (I) is useful in gene therapy techniques to restore normal consequences of the investigation of (II) or to treat disease states involving (II). (II) is consequenced in tissue, as molecular weight markers and as a food consupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The collapsettice and polynucleotide sequences have applications in consisting forensics, gene mapping, identification of mutations constituted sequences have applications in the produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this consistency of the invention of the sequence of the invention of the sequence of the invention of the collapse of the invention of the sequence of the invention of the collapse of the invention of the collapse of the collaps
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167
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                                                      Sequence 1668
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                                                         BP; 571 A;
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                                                                                            21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
                                                                                                                  GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                               AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                             AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
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517.00
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Matches:
Conservative:
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Indels:
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98
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81

| IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98

GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG

80 204 60

264

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RESULT 7
AAD40085
ID AAD4
XX AAD4
XX AAD4
XX AAD4
XX Huma
XX Huma
XX Huma
XX Huma
XX Infil
XX
       CC The invention relates to an isolated polypeptide comprising a death cf domain (DD), death effector domain (DD) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC (CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent, DED or NB-ARC (CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent, CC period of the association of the domain and the candidate binding agent, CC period of a cell process such as cell proless to microbial infection and B cell evel of a cell process such as cell proless within a cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell candidate binding agent, CC immunoglobulin class switching, in particular apoptosis within a cell entibody specifically reactive with CTDD DD of C. trachomatis, C. CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The CC invention is useful for modulating the activity of oncogenic proteins, CC crowdiary a pathology caused by the oncogenic proteins and for treating a pathology caused by the oncogenic proteins and for creating bacterial infections by modulating the activity of bacterial for cliscovery of drugs that suppress infection, inflammation, allergy, caused by the oncogenic proteins and for treating a pathology caused by the oncogenic proteins and for creating bacterial infections by modulating the activity of bacterial for cliscovery of drugs that suppress infection, inflammation, allergy, caused by the oncogenic proteins and for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, fibrosis, the cell division, inflammatory diseases such as sepsis in the complete comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Page 194-196; 209pp; English..
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P-PSDB; AAE24865.
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iewen F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
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RESULT 8
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis death domain containing protein; fibrosis; sepsis; neural growth factor receptor-interacting death domain; cell adhesion; vasotropic; microbial infection; hiflammation; allograft rejection; CTDD cell stress response; benign prostatic hypertrophy; antibacterial; NIDD; apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy; neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic; keloid; interleukin-l receptor-associated kinase; IRAK; gene; ss.
  (REED/)
(GODZ/)
(PAWL/)
(FIOR/)
(LEES/)
                                                                                                                                                                    17-NOV-2000;
17-NOV-2000;
                                                                                                                                               29-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; death Domain; DD; death effector domain; DED; cell proliferation;
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GODZIK A.
PAWLOWSKI K.
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  LEE S H.
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides novel death Domain (DD) and death effector CC domain (DED) proteins and nucleic acids encoding them. The invention also CC provides death domain containing protein such as Chlamydia trachomatis CC death domain containing protein (CTDD) DD and neural growth factor CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED or NB-ARC domain and identifying an effective agent (e.g. protein or drug) that binds the DD, DED or NB-ARC domain. The invention is also useful for CC that binds the DD, DED or NB-ARC domain. The invention is also useful for CC modulating the level of cell process such as apoptosis, cell adhesion, CC cell proliferation, cell immunoglobulin class switching. DDs, DED and NB-ARC domain and B cell immunoglobulin class switching. DDs, DED and NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allograft rejection, sepsis and other diseases. CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, allograft rejection, sepsis, keratinocyte inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC inflammatory hyperplasia and smooth muscle cell proliferation in arteries CC interfeuxing balloon angloplasty (restenosis). The invention is also used in interleuxin-1 receptor-associated kinase (IRAK)-4 full length gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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P-PSDB; AAE38908.
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GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 133 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20

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US-10-001-254-6 (1-98) x ACC47548
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                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                      Alignment Scores:
                                                                                                                                                                         The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-4, specifically hybridising with the nucleic acid and inhibiting the expression of the encoded product. Also disclosed is the compound hybridising with an 8-nucleobase portion of an active site on a nucleic acid molecule encoding IL-1 receptor-associated kinase-4. The antisense oligonucleotide is useful for treating an animal having a disease or conditions associated with IL-1 receptor-associated kinase-4, e.g. cancer (particularly renal cancer), inflammatory disease or an infection. The antisense compounds are useful for diagnostics, therapeutics, prophylaxis, or as research reagents or kits. The current sequence represents the human IL-1 receptor-associated kinase-4 encoding sequence (GenBank accession number NM_016123)
                                                                                                                                                                                                                                                                                                                                                                                                  Example 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides for modulating IL-1 receptor-associated kinase-4 gene expression, particularly useful for preventing, delaying treating e.g. cancer (e.g. renal cancer), inflammatory disease or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
                                                                                                         No.:
                                                                                                                                                    Sequence 2817 BP; 912 A; 547
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The present sequence is a cDNA encoding human interleukin (IL)-1 r associated kinase (IRAK)-4. IRAK associate with activated IL-1, II other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respira
                                                                                                                                                                                                                                                                                                       Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer.
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                                                                                                                                                                                                                                               Claim 7; Fig 2; 89pp; English.
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Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II, antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus crythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis;
                                                                                                                                                                                                                                                                                                                                          Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
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conhibitors are useful for treating inflammatory diseases such as commonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), company fibrosis, interstitial lung disease, asthma, chronic cough or callergic rhinitis), transplant rejection, autoimmune diseases (e.g., creation of arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), correct diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), correct diabetes), cancer (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), cD14 corrected sepsis, non-CD14 mediated sepsis, osteoparthritis, osteoporosis, corrected dermatitis), inflammatory bowel disease (e.g., Crohn's disease and conditions of activity or expression are used to inhibit signal transduction cresulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription of activation of activates NFkappaB in the cell. IRAK-4 is used to create a condumnant transgenic animal which is useful for testing the function of a transcription of activates and conditions and for the development of potential treatments corrected inflammatory diseases and conditions. IRAK-4 sequences are consistent than the cell of the study of inflammatory corrected inflammatory and incare the activation of a transcription of a corrected inflammatory diseases and conditions. IRAK-4 sequences
                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF) kappaB activation. The IRAK-4
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                                                                                                                                                  Sequence 1542
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                     Match:
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)B; AAE05399.
                                     Similarity:
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21-UN-2000; 2000US-021361P.
01-SEP-2000; 2000US-0223763P.
05-SEP-2000; 2000US-0230629P.
14-SEP-2000; 2000US-023265P.
19-DEC-2000; 2000US-0257037P.
08-JAN-2001; 2001US-0260796P.
The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells specific for a tumour protein. The composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung tumor polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                DNA encoding
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             biodiversity.
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DB; ABG12616.
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                                                                                                                                                                                                            Antisense therapy; cytostatic; antimicrobial; antiinflammatory; interleukin-1 receptor-associated kinase-4; human; cancer; renal cancer; inflammatory disease; infection; diagnostic; therapeutic; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                         ACC47549;
              28-SEP-2001; 2001US-00966451
                                                                                                                                                                                                                                                                                 Human DNA complement sequence # SEQ
                                                                                                                                                                                                                                                                                                                                                                                           ACC47549 standard; DNA; 31000 BP
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                                                  26-SEP-2002; 2002WO-US030574
                                                                                                                       WO2003028636-A2
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                      11-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31000 BP; 9247 A; 5856 C; 5924 G; 9973 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a compound of 8-50 nucleobases which is targeted to a nucleic acid encoding interleukin-1 (IL-1) receptor-associated
                                                                                                                                                                                                                                                                                                               NB-ARC
                                                                                                                                                                                                                                                                                                                                                                                                           Human IRAK4 short gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD40084 standard; DNA; 211
                                                                                                                                                                                                  NNB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
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                                                                                                                                                                                                                                                                                                                                        death domain; DD; death effector domain; DBD; Chlamydia infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe
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                                                                                                                                                                                                 US-10-001-254-6 (1-98) x AAD40084
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 211 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 195; 209pp; English.
                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy and
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29-JUN-2001; 2001US-0301889P
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  41
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                                                                GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
AsnGlnPheHisIleArg
                                       ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                               ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                  77 A; 41 C;
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Search completed: January 12, 2005, 07:14:08 Job time : 421 secs

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Result
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-Q=/Ggn2_1/USPTO_spool_h/US10001254/runat_10012005_172739_10471/app_query.fasta_1.263
-Q=/Ggn2_1/USPTO_spool_h/US10001254/runat_10012005_172739_10471/app_query.fasta_1.263
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMAYCH=0.1 -LCOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TPRANS=human40.cdi -LIST=45
-DCCALIGN=10 -THR_SCORE=pCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LCCAL
-OUTFMT=ptc -NOMM=ext -HEAPSIZE=560 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001254 @CGN 1.1_3437 @runat 10012005_172739_10471 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPB_LCCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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BQ552228 H4014C09-
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77	082	9505	36	65604 6407	BJ691338 BJ691338	76165 BX87616	75297	93 CR37009	52 BJ03596	5 AL6471	06 BL0081	35 TCBAP1	52 Ag2_p	CN061000 A22 Ag2 p	10 K20_Ag2	97 F20_Ag2	Ξ	7581 7	3616 AJ45	L1 6039508)349 BB86	5	1069 340084	3793 Mus musc	60 um23	8792 Pan trog	18791 Homo	22921 BX52	9028 Mus	288	ဒ	3167 BB61316	Y726858 BY72685	Y7215	

ALIGNMENTS

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	source	FEATURES								COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			OBCANTOM	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BG164491	PESIT.T 1
/CIDILE="INAGE:4452055"	/Organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /lb_xref="taxon:9606"	High quality sequence stop: 634. Location/Qualifiers	Plate: LLAM10240 row: d column: 08	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	DNA Commencing by: The I.M.A.G.E. Consortium (HENE)	cDNA Library Preparation: Life Technologies, Inc.	Tissue Procurement: ATCC	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	HOMO Sapiens (Iuman)		BG164491.1 GI:12671194	BG164491	mRNA sequence.	6F1 NIH MGC 89 Homo sapiens cDNA clone IMAGE	BG164491 859 bp mRNA linear EST 06-FEB-2001		

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                                                                              Single pass sequencing. Bases called trimmed with the aid of the trim_alt cross_match v0.990329.
Plate: TMW8032 row: K column: 23 Seq primer: GTAATTACGACTCACTATAGGG.
                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 821)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library coembryos representing early developmental stages unpublished (2003)
                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                   Contact: Smith TPL
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/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="hypernephroma, cell line"
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/clone lib="NIH MCC_89"
/clone lib="NIH MCC_89"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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SOURCE KEYWORDS 밁 Ś

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                                                                                                                                                                                               CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                     Plate: LLCM1645 row: p column:
High quality sequence start: 3
High quality sequence stop: 613.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUG616438 811 bp mRNA linear EST 18-APR-2001 602642772F1 NIH_MGC_61 Homo sapiens cDNA clone IVAGE:4773760 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
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RESULT 4
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                                                                                                                                                          Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index

Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE482619 402 bp
168463 BARC SBOV Bos taurus cDNA
BE482619
                                                        Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cow)
                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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    (bases 1 to 402)

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301 504 8414
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/note="forgan: testis; Vector: pDNR-LIB (clontech); Site_1:
/note="forgan: testis; Vector: pDNR-LIB (clontech); Site_1:
SfiI (ggccgctctggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
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Functional Genomics Lab

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                                                                                                                                                 Bos taurus
Bos taurus
                                                                                                                                                                               sequence.
CN788062
CN788062.1
EST.
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Unpublished (2004)
Contact: Richard G. Baumann
                          1 (bases 1 to 666)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S.,
Matukumalli, L.K.
Construction and Analysis of a cDNA Library (
Intestinal Muscle and Epithelial Tissues of )
                                                                                                                                                                                                                                           CN788062
4122347 BARC 8BOV
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 11 row: F column: 7
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e.\ Vector\ identified\ by\ cross_match\ with\ the\ -minscore
                                                                                                     Mammalia; Eutheria;
Bovinae; Bos.
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                                                                                                                                     Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                    GAGTTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab host="DH10B"
/lab host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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495.00
97.96%
93.88%
95.74%
                                                                                                                                                                    (cow)
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                                                                                                                     Cetartiodactyla; Ruminantia;
                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Conservative:
Mismatches:
Indels:
Gaps:
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8BOV_26007
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0 0 2 4 0 2
                              Generated From Holstein Cattle
                                                                            Van
                                                                            Tassell, C.P.
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5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                     BF696981
                            Homo sapiens
                                          Homo sapiens (human)
                                                                              BF696981.1 GI:11982389
                                                                                                                mRNA sequence.
                                                                                                                                 602130160F1 NIH_MGC_56 Homo
                                                                                                                                                        BF696981
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Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=Toran: Intestine; Vector: pCMVSport6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Bpithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab host="DH10B TonA"
/clone_lib="BARC 8BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
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sex="Female"
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495.00
97.96%
93.88%
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Matches:
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TITLE
JOURNAL
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CA538859 TRNA linear EST 19-NOV-2002 C0272B01-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:C0272B01 IMAGE:30017484 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1124 row: g column: 15
High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                 GAATTACTGGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTGGTGGATCTTTT
                                                                                                                                                                                                                                              GluLeuLeu-PheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLe 80
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                               GATCCAAAATGAATTTGTTGGCTCCTGCAAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                                                                                                                                                                                                                      AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCCACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="primitive neuroectoderm"
/lab host="DH10B (T1 phage-resistant)"
/clone_ilb="NH10B (T1 phage-resistant)"
/clone_ilb="NH MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcggctcggcc); Site_2: Sfil (ggcgattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5;
and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCAGGGCGGCCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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485.00
97.00%
97.00%
93.81%
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                   387
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                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                    211
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ACCESSION
VERSION
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           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                     Score:
                                                                              Alignment
                                                                                                           ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                    No . .
                                                                                Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Other_ESTs: C0272B01-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Tanaka,T., Lim,M.K.,
Luo,A. and Ko,M.S.H.
Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: C0272 row: B column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA538859.1 GI:25080828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmalia; Eutheria; (bases 1 to 503)
                                                                                                                              quality sequence stop: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NIA:C0272B01 IMAGE:30017484"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="niaEST:C0272B01-5N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
  1.56e-54
476.00
95.92%
90.82%
92.07%
                                                                                                                       Yulan Piao (NIA)."
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Rodentia;
                                                    Length:
Matches:
              Mismatches:
Indels:
                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
0 4 5 9 3
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SOURCE ORGANISM VERSION KEYWORDS

Mus musculus

Mus musculus (house mouse) BQ552228.1 GI:21453114

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 598)

VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Kasembly, verification, and initial annotation of NIA 7.4K mouse

Mus.

HITLE

RESULT 8 BQ552228

DEFINITION ACCESSION

598 bp mRNA linear EST 20-JUN-21 H4014C09-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4014C09 5', mRNA sequence.

EST 20-JUN-2002

밁 Ś 밁 S 밁 Ś 밁 8 . 늄

372

312

192

61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80

GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG

431

41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60

ANTCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT 371

21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40

CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAAGCCGTCCGGCGACGACAGATAC 311

Alignment Scores:			
Pred. No.:	1.98e-54	Length:	598
Score:	476.00	Matches:	89
Percent Similarity:	95.92%	Conservative:	ຫ
Best Local Similarity: 90.82%	90.82%	Mismatches:	4

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strain="C57BL/6"

type="mRNA"

clone="H4014C09"

sex="mixed"

/organism="Mus musculus" /mol_type="mRNA" Location/Qualifiers

FEATURES

Seq primer: -21M13 Reverse High quality sequence stop: 598 POLYA=No.

Contact: Yong Qian
Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4014 row: C column: 09

Bource

.598

COMMENT

MEDLINE JOURNAL PUBMED

Genome Res.

12 (12), 1999-2003 (2002)

cDNA clone set

12466305

22354164

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US-10-001-254-6 (1-98) x CA538859 (1-503)

 ${\tt ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro}$

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RESULT 9
BB660378
LOCUS
DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #16 GTCCAGATTGAGCTGTTTGCCCCCGCCACTCTGCTGCTGCCGGATGCCGTTCCCC
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genom Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 610)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ico,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
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Unpublished (2001)
                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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BB660378.1 GI:16494199
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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RESULT 10
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DB:
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Best Local Similari
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                                                                                                                                                                                                                                                  332
                                                                                                                                                                                                                                                                                                            272
musculus cDNA clone 4
BB613447
BB613447.1 GI:164540
EST.
                                                                                                                                  452
                                                                                                                                                                                      392 GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
                                                                                                                                                                                                                                                                                                                                                                     212
                                                                                                                                                            81
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                                                        BB613447
BB613447
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                                                                                                                          IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                      GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                                                                                                                                                                                                                AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                                                                                              AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCACCTGT
                                                                                                                                                                                                                                                                                                                          GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                                                                                                                                                                                                                                                                 ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                  ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                    637 bp ml
RIKEN full-length enriched,
cDNA clone 4732482P03 5', ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="lung"
/dev_stage="13 days embryo"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watshirki, K., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA concentration of an encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                       prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 10 day neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="mixed"
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Rodentia;
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ACCESSION VERSION KEYWORDS RESULT 11 BY721552 片 á 片 S 片 S 밁 Ş 片 δ Alignment Scores: Pred. No.: Score: REFERENCE SOURCE DEFINITION rocus US-10-001-254-6 (1-98) x BB613447 Best Local Similarity: Query Match: Percent Similarity: ORGANISM AUTHORS Notaces 1 Co. 100 No. N. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Chothia, C., Corbani, T.B., Schonbach, S., Dalla, E., Dragani, T.A., Pletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Garimond, S., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Glustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Waltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pillai, R., Pontius, J. U., Oj, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J. U., Oj, D., Ramachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane, K., Shiraki, T., Waki, K., Kawai, J., Alizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., 373 313 193 433 253 CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAGATAC 312 81 61 41 21 GlnGluGlyTrpLygLygLeuAlaValAlaIleLygLygProSerGlyAgpAgpArgTyr 40 BY721552 BY721552 BY721552.1 EST. Mammalia; Eutheria; Mus musculus musculus Eukaryota; Metazoa; Mus musculus (house mouse) IleGlnAsnGluPhePheAlaProAlaSerLeuLeuProAspAlaValPro GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60 ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT GTCCAGATTGAGCTGTTTGCCCCCCCCCCACTCTCCTGCCGGATGCCGTTCCC AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT 372 GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro (bases 1 to 638) 638 bp mRNA linear RIKEN full-length enriched, adult male of CDNA clone 9330209D03 5', mRNA sequence 2.15e-54 476.00 95.92% 90.82% 92.07% GI:27134669 Chordata; Rodentia; (1-637) Mismatches: Indels: Gaps: Length: Matches: Conservative: Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. mRNA linear EST 17-DEC-2002 1, adult male diencephalon Mus 486 98 80 432 252 20

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.
Please visit our web
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="RIKEN full-length enriched, adult male
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/dev_stage="adult"
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                  TITLE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 63)

RE 1 (bases 1 to 63)

RS (okazaki,Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazet, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinsoich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagshima, T., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Kund, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation
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BY726858.1
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RIKEN full-length enriched, adult male corpora quadragemina Mus musculus cDNA clone B230034I03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCAGTTCCATATAAGGAGATTCGAAAGCCTTACTTCAGACCGGGAAGAGCCCCACCTGT
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95.92%
90.82%
92.07%
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COMMENT
                                       Pred. No.:
Score:
                                                                                               Alignment Scores:
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MEDLINE
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                   quadrigemina"
                                                                                                                                                                                                                         modified pBluescript KS(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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2.28e-54
476.00
95.92%
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                                Length:
Matches:
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAGATAC
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Fatuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takada, Y., Tanka, T., Toya, T., Muramatsu, M. Takahashi, F., Takada, Y., Tanka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,X., Itoh,M., Konno,H., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watahiki,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB613167 mRNA
BB613167 RIKEN full-length enriched, 10
musculus cDNA clone 4732460109 5', mRNA
                                                                                                                                                and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                         IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuDroAspAlaValPro
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                                                                                            GTCCAGATTGAGCTGTTTGCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCCC
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/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched,
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/clone="4732460109"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                              Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Harajaki, T., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, X., Sano, H., Sagaba, Y., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Voshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Gen Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                   On Oct 4, 2001 this sequence version replaced gi:12860970. Please visit our web site (http://genome.gsc.riken.jp/) fc
                                                                                        URL:http://genome.gsc.riken.jp/,
Fax:81-45-503-9216)
                                                                                                                                                                                                                           Submitted (18-AUG-2000) Yoshihide Hayashizaki,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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6 (bases 1 to 1161)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK028837

2481 bp mRNA linear HTC 03-APR-2004
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
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                                                                                                                 GTCCAGATTGAGCTGTTTGCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCCC
                                                                                                                                                             IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
                                                                                                                                                                                                                                                    GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
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DAVPQTVKSLPPKEAGNSGTNTRALSGKGQDIRNAYAKTRTQLRATGLLSPDNRSVES
SDTRFHSFSFHELKSITNNFDEQPASAGGNRWGEGGF"
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receptor-associated kinase 4 (Mus musculus)
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/protein_id="BAB32090.2"
/db_xref="GI:15919912"
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/db_xref="taxon:10090"
/clone="9330209D03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain="C57BL/6J"
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                                                                                                                           AL Nature 420, 563-573 (2002)

CE (bases 1 to 2481)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., RS Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Radachi, J., Furuno, M., Hanagaki, T., Haraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nachi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Jirect Submission

Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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kinase 4
AK028837
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Genome
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Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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[Mus musculus], full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlnGluGlyTrpLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
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GTCCAGATTGAGCTGTTTGCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
                                                                                                                                                                                                                                                                                                           AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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receptor_associated kinase 4 [Mus musculus]
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
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/mol_type="mRNA"
/strain="C57BL/6J"
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'db_xref="taxon:10090"
'clone="4732460I09"
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-DB=!ssued_Patents_NA_-QFMT=fastap_SUFFIX=p2n.rni-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001254 @CGR_SCORES=0 -NORD=1001254 @CGR_SCORES=0 -MAIT_-DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Ygapop 10.0 , Ygapext
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US-09-863-549-1
US-09-307-185-3
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US-09-773-753-1
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51, Appl
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576, Ap
 6, Appl:
4327, Ap
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Sequence 3. Application US/09966451
; Sequence 3. Application US/09966451
; Patent No. 6632959
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL.
; FILE REFERENCE: RTS-0324
; CURRENT APPLICATION NUMBER: US/09/966,451
; CURRENT FILING DATE: 2001-09-28
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Best Local Similarity:
Query Match:
DB:
US-09-966-451-10
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SEQ ID NO 3
LENGTH: 2817
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LOCATION: (50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                            254
                                                                                                                                          194 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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Best Local Similarity:
Query Match:
                                                             US-10-001-254-6 (1-98)
                                                                                                                                                            Alignment Scores: Pred. No.:
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; LOCATION: (64)..(1851)
US-09-135-232-1
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Best Local Similarity:
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Patent No. 628228
GEMERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/135,232
CURRENT FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2288
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4
FILE REFERENCE: RTS-0324
CURRENT APPLICATION UNMEER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 31000
                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: human
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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                ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeu 27
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98.00%
49.52%
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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Sequence 1, Application US/09863549

Patent No. 6576444

GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
ITILE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
TITLE OF INVENTION INDEER: US/09/863,549

CURRENT APPLICATION NUMBER: US/09/863,549

CURRENT APPLICATION NUMBER: 09/135,232

PRIOR APPLICATION NUMBER: 09/135,232

PRIOR APPLICATION NUMBER: 09/135,232

PRIOR APPLICATION NUMBER: 09/135,232

PRIOR PILLING DATE: 1998-08-17

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 2288
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Best Local Similarity:
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                                                                                                                                        Sequence 1, Application US/08980060 Patent No. 5965421
                                                                                                                         GENERAL INFORMATION:
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ORGANISM: human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (64)..(1851)
APPLICANT: MUZIO, MAR
APPLICANT: DIXIT, VIS
TITLE OF INVENTION: H
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . No.:
                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                          196 GCAGAGAGACTTTCAAGC----------AGCTGGCTGGATGTTCGTCAT 234
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                                                                                                                                                                                                                                             CAGAAAAACAAGACCATCGGTGACCTTTTACAGGTCCTC 333
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                                     NI, JIAN
FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.000102
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31.51%
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                       HUMAN IRAK-2
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; Sequence 1, Application US/09307185; Patent No. 6222019; GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING; PING; PAPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2; NUMBER OF SEQUENCES; 14
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Best Local Similarity:
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US-08-980-060-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEFFE, ERIC K.
REGISTION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
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CORRESPONDENCE ADDRESS:
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STREET: 1100 NEW
CITY: WASHINGTON
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 CTGCGGAAGATCAAGTCCATGGAGCGGTGCAGGGTGTGAGCATCACGCGGGAGCTGCTG 216
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Matches:
Conservative:
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Indels:
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RESULT 8
US-09-773-753-1
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Best Local Similarity:
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US-09-307-185-1
                                             Sequence 1, Application US/09773753
Patent No. 6653452
GENERAL INFORMATION:
APPLICANT: NI, JIAN
FENG, PING
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REGISTRATION NUMBER: 1488
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TOTROHOME: (202) 371-2600
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NAME/KEY:
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION: HUMAN IRAK-2
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          MUZIO, MARTA
DIXIT, VISHVA M.
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Matches:
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RESULT 9
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Best Local Similarity:
Query Match:
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                                                    Sequence 3, Application US/08980060 Patent No. 5965421
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
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COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/99/773,753
FILING DATE: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: 08/980,060
APPLICATION NUMBER: 08/980,060
APPLICATION NUMBER: 36,688
APPLICATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
REGISTRATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
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LENGTH: 1806 base pairs
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
                                                                                                                                   337 CCCATTCCAGCCTTCCCTGACTCTGTG
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STRANDEDNESS: double
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ZIP: 20005-3934
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Matches:
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RESULT 10
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                                                                    Sequence 3, Application US/09307185 Patent No. 6222019
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vc
SOFTWARE: Patentin Release #1.0, Vc
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEPPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                APPLICANT: NI, JI
APPLICANT: FENG,
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TELEFAX: (202) 371-540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
 APPLICANT:
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TOPOLOGY: lii
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NI, JIAN
PENG, PING
MUZIO, MARTA
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DIXIT, VISHVA M.
VENTION: HUMAN IRAK-2
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Matches:
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Indels:
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RESULT 11
US-09-773-753-3
Sequence 3, Application US/09773753
Patent NO. 6653452
GENERAL INFORMATION:
APPLICANT: NI, JIAN
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Best Local Similarity:
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ATTORNEY/AGENT INFORMATION:
ANAME: STEFFE, ERIC K.

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DIXIT, VISHVA M. TITLE OF INVENTION: HUMAN I NUMBER OF SEQUENCES: 14
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3459 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
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Matches:
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Indels:
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RESULT 12
US-08-980-060-14/c
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Best Local Similarity:
Query Match:
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Sequence 14, Application US/08980060
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/773,753

FILING DATE: 02-Peb-2001

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/980,060
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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LENGTH: 3459 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
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ADDRESSES: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                   217 TGGTGGTGGGGCATGCGGCAGCCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG
                                                                       337 CCCATTCCAGCCTTCCCTGACTCTGTG 363
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                                                                                                                                             GAGCTCTACCGGGCTGCCCAGATCATCCTGAACTGGAAACCGGCTCCTGAAATCAGGTGT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202)
TELEFAX: (202) 37
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DIXIT, VISHVA M.
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15.28%
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371-2540
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Matches:
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; Sequence 14, Application US/09307185
Patent No. 6222019
; GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 479 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
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APPLICANT: EENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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                                                                                                                                                                                                                         124 GAGCTCTACCGGGCTGCCCAGATCATCCTG
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                                                                                                                                                                                                                                                                                               184 TGGTGGTGGGGGATGCGGCAGGCCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG 125
                                                                                                                                                                                                                                                            84 GluPhePheAlaProAlaSerLeuLeuLeu 93
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38.00%
15.18%
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Matches:
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Best Local Similarity:
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                                                                                                                                                                         Sequence 14, Application US/09773753
Patent No. 6653452
GENERAL INFORMATION:
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RANGE STEPPE, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2640
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE:
CLASSIFICATION:
DBTCD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
                                                                                                                                                           APPLICANT: NI, JIAN
                                                                                         TITLE OF INVENTION: HUMAN IRAK-2
                                                                                                                                                                                                                                                                                   124
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/980,060
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1488.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/773,753
FILING DATE: 02-Feb-2001
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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Search completed: January 12, 2005, 08:54:30 Job time: 157 secs
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Score: 72.00
Percent Similarity: 47.06%
Best Local Similarity: 32.94%
Query Match: 13.93%
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; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1
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Pred. No.:
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Matches:
Conservative:
Mismatches:
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Gaps:
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Command line parameters:

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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_spool_h/US10001254/runat_10012005_172738_10459/app_query.fasta_1.263
-DB=GenEmb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LŌOPCL=0 -LŌOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER-US10001254_@CGN 1_1_3731_@runat_10012005_172738_10459 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

	CDS			source	FEATURES		JOURNAL	TITLE		AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AA431296
/note="unnamed protein product" /codon_start=1 /protein_id="CAD37274.1" /db_xref="GI:21656166" /translation="TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFH	<1>294	/mol_type="unassigned DNA" /db xref="taxon:9606"	/organism="Homo sapiens"		Location/Qualifiers	BURNHAM INST (US)	Patent: WO 0240680-A 5 23-MAY-2002;	Novel death domain proteins	Roth, W. and Stenner-Liewen, F.	Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX431296.1 GI:21656165	AX431296	Sequence 5 from Patent WO0240680.	AX431296 294 bp DNA linear PAT 28-JUN-2002	

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Scanlan, M.J., Stockert, E., Chen, Y.-T., Old, L.J., Jager, E.
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                             GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspAspArgTyr
                                                          ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                    ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
\tt AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
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/mol_type="genomic
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AX431306
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Sequence
AX431306
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Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens
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                                                                                                              GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                    AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                   AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                                               ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                                                                                                                                                              ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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1383
                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MMKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDBTXYNQFHIRREALLQTGKSSFTSELLFDWGTTNCTVGDLVDLLIQNEEFAPASLLLPDWGTKTANTLPSKEAITVQQKQMPFCDKDRTLMTPVQNLEQSYMPPDSSSPENKSLEVSDTRFHSFSFYELKUNTNNFDERFISVGSNKWGEGGFGVVYKGYVNNTTVAVKKLAAM VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSCLDGTPFLSWHRCKLAQGAANGINFLHENHHHHDIKSANILLDEAFTAKISDEGLAR ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE PQLLLDIKERIEDEKTIEDYIDKKWNDADSTSVEAMYSVASQCLHEKKNKRPDIKKVQADQLLQEMTAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
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                                                                                                                                                                    Bource
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences
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                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 19 Row: n Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) NA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, An Madan, Jessica Fahey, Erin Helton, Mark Ketteman, And Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R
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human and mouse cDNA sequences
brace Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1629 bp mRNA linear PRI 30-JUN-2004
Homo sapiens interleukin-1 receptor-associated kinase 4, mRNA (cDNA
clone MGC:13330 IMAGE:4287014), complete cds.
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/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone="MCG:13330 IMAGE:4287014"
/tlssue_type="srain, primitive neuroectodermal"
/clone_Ib="NIH_MGC_56"
                                                                                                                                   organism="Homo sapiens"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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and Michelle Whiting
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AUTHORS
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US-10-001-254-6 (1-98) x BC013316 (1-1629)
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Best Local Similarity:
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Human interleukin-1 receptor associated kinase 4 cDNA sequences Unpublished 2 (bases 1 to )676'
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1636)

Chuang,T.H. and Ulevitch,R.J.
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                           AY340962.1 GI:37727958
                                                                                                                                                                                                                                                                                   Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4) mRNA, complete cds; alternatively spliced.
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DAVPKTANTLPSKEAITVQQKGMPFCDKDRTLMTFVQNLEQSYMPPDSSSPENKSLEV
SDTRFHSFS FYELKNVTINNFDER PISVGGNKGLEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQBIKVMAKQQHBNLVELLGFSSDGDDLCLVYVYMSSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAXISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPBALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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/db_xref="GI:15426432"
/db_xref="LocuBID:51135"
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                                                                                                                                                                     Homo sapiens interleukin-1 receptor-associated kinase 4 variant (IRAKA) mRNA, complete cds; alternatively enliced
                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                           AY340963.1
                                                               Homo sapiens (human)
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DDRYNGPHIRREALLOTGKSFTSELLEDWGTTNCTVGDLVDLLIQNEFFAPASLLLE
DAVFKTANTLSSKEAITVQQKQMFGCDXGRTHMTPVQNLQGYMPFDSSSEEMSLEV
SDTRFHSFSFYBLLVTVNVFDERFISVGGNKMGEGGFGVVYKGYVNNTTVAFXKLAFAV
VDITTEBLKQQFDQEIKVMAKCQHENLVTLLFFSSGGDLDLCLYYVYMFBGSLAFXLDRLSC
LDGTPFLSWHMCKIAQGAANGINFLHENHHIHRDIKSAULLDAFFINGSLLDRLSC
LDGTPFLSTALAGGAANGINFLHENHHIHRDIKSAULLDEAFTATISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAFBALLGGITFSCHAFTATISDFGLAR
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/product="interleukin-1 receptor-associated kinase
/protein_id="AAR02358.1"
/db_xref="GI:37727959"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
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Chuang, T.H. and Ulevitch, R.J.
Direct Submission
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Chuang, T.H. and Ulevitch, R.J.
Human interleukin-1 receptor
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                                                                                                                 | IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
                                                                                                                                                                                     GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                                                                                                                  GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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                                                                                          ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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2775 bp DNA
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/gene="IRAK4"
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SDTRFHSFSFYELKNVTNNFDERFISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTELKQOFDQEIKVMAKQQHENLVELLGFSSGDDLCLVYVYMPMSGLLDRLSC
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LDGTSPLSWHRTCKIAQGAANGINFLHENHHIRDIKSAULLDRLSC
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/db_xref="taxon:9606"
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/db_xref="GI:37727961"
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/codon_start=1
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AR475548
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ORGANISM
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                            Patent: US 6692959-A 3 17-FEB-2004;
Location/Qualifiers
1. 2817
                                                                                    1 (bases 1 to 2817)
Bennett, C.F. and Freier, S.M.
Antisense modulation of IL-1 receptor-associated kinase-4
                                                                                                                                                Unknown
                                                                                                                                                                                                       Sequence 3
AR475548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 02068579-A 14314 06-SEP-2002; PE Corporation (NY) (US)
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQ728380
CQ728380.1
                                                                                                                                 Unclassified.
                                                                                                                                                             Unknown.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                    GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="unknown"
/mol_type="genomic
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patent US 6692959.
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Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                               Roth, W. and Stenner-Liewen, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Sequence 27 from Patent
AX431318
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX431318.1 GI:21656187
                                                                                                                                                                                                                                                                                                                                                                                      Pawlowski, K., Fiorentino, L.,
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                                                                                                          /protein_id="CAD37285.1"
/db_xref="GI:21656188"
                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                                                                                                                                                                                                                                                 note="unnamed protein product"
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AF155118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2817)
Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,E.,
Jongeneel,V., Gure,A.O., Jager,D., Jager,E., Knuth,A.,
and Old,L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigens recognized by autologous antibody in patients with renal-cell carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scanlan, M.J., Gordan, J.D., Williamson, B., Stockert, E., Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., and Old, L.J.
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1 (bases 1 to 2817)
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                             /product="putative protein kinase NY-REN-64 antigen"
/product=in_tid="AAD142884.1"
/protein_id="AAD142884.1"
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/db x
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/mol type="mank"
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/cell type="renal cell carcinoma"
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se NY-REN-64 antigen mRNA,
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Chen, Y.-T.
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Chen, Y.-T.
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                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 2820)
2 (bases 2 to 2820)
3 (suguno, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission

Direct Submission

Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspAspArgTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Ta Nakamura, Y., Isogai, T. and Sugano, S.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="KAT"
                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10395"
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Tanaka, T.,

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4.
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Medvedev,A.E., Lentschat,A., Kuhns,D.B., Blanco,J.C.G.,
Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to
Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                 1381 bp m Homo mapiens interleukin-1 receptor 2 (IRAK4) mENA, complete cds.
Direct Submission
Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD 21201-1559, USA
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                 Medvedev,A.B., Lentschat,A., Kuhns,D.B., Blanco,J.C.G., Salkowski,C., Zhang,S., Arditi,M., Gallin,J.I. and Vogel,S.N.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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Exp. Med. (2003) In press
(bases 1 to 1381)
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/db_xref="GI:7020684"
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Eukaryota; Metazoa; C
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Sequence 2 from Patent WO0151641.
AX196260
Wesche, H. and Li,S. Irak-4: compositions and methods of use
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/replace="ac"
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SDTRPHSPSPYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNNCGSEEACSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="IRAK-4 mutated form 2; truncated protein kinase due to frameshift and premature stop codon caused by deletion of positions 620-621 in the wild-type coding region"
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/mol_type="mRNA"
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1. .1381
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                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                  Homo sapiens interleukin-1 receptor associated kinase mRNA, complete cds.
                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  IRAK-kinase
                              IRAK-4: a novel member of the
                                      1 (bases 1 to 1383)
Li,S., Strelow, A., Fontana, E.J. and Wesche, H.
                                                                                   Homo
                                                                                           Homo sapiens (human)
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        Natl. Acad. Sci. U.S.A. 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-NOV-2001) Biology I,
South San Francisco, CA 94080, USA
Location/Qualifiers
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Li,S., Strelow,A., Fontana,E.J. and Wesche,
Direct Submission
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/protduct="intearleukin-1 receptor associated kinase 4"
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VDITTEELKQQFDQFIKWAKCQHENLYWELLGFSSDGDDLCLTVYVYNENGSLLDRLSC
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ASEKFAQTVWTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEITTGLFAVDEHRE
PQLLLDIKEEIEDEEKTIEDYIDKKWNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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/note="protein kinase"
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mRNA

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8 8		US-10-001-254-6	Alignment Sc Pred. No.: Score: Score: Percent Simi Best Local S Query Match: DB:	ORIGIN					CDS	gene				FEATURES	TITLE JOURNAL	AUTHORS	JOURNAL	TITLE	AUTHORS	PRESENCE	SOURCE ORGANISM	VERSION VERSION	DEFINITION
25 ACAIAIGIGCGCIGCCICAAIGIIGGACIAAIIANGAAGCIGICAGAIITTAIIGAICCI 84 21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40	ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro	54-6 (1-98) x AY283670 (1-1383)	ment Scores: 3.24e-60 Length: 1383 . No.: 513.00 Matches: 97 snt Similarity: 98.98% Conservative: 0 Local Similarity: 98.98% Mismatches: 1 Local Similarity: 99.23% Indels: 0 Match: 99.23% Gaps: 0		DDRYNGHIRRFEALLQTGKSPTSELLEPWGTTNCTAGDIJCHE ALEGENAAM VALAGE OF DDRYNGHIRRFEALLQTGKSPTSELLEPWGTTNCTAGDIJCHLILLEFRAPASLLLP DAVPKTANTLPSKEAITVQQKQMPFCDKDRTLMTPVQNLEQSYMPPDSSSPENKSLEV SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM VDITTEELKQQFDQSIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC LDGTPPLSWHMRCKIA"	/protein_id="AAP57089.1" /protein_id="AAP57089.1" /bb xref="GI:31871818" /rep==1=4:0n="MANDSTREET NUCTIENT CRETTEDOROUSET AVAIVABGG	<pre>/codon_start=1 /product="interleukin-1 receptor associated kinase 4 mutant form 1"</pre>	<pre>/gene="IRAK4" /note="IRAK-4 mutated form 1; truncated protein kinase due to premature stop codon"</pre>	1879	/note="genotype: compound neterozygous" 11383 /cone_"Tabk4"	lipopolysaccharide and interleukin-1 and suffering from recurrent bacterial infections" /db xref="taxon:9606"	/osgration source="patient hyporespaonsive to	11383/	21201-1559, USA Location/Oualifiers	Direct Submission L Submitted (25-APR-2003) Microbiology and Immunology, University of Maryland, Baltimore, 655 West Baltimore Street, Baltimore, MD	Med Vedeve, R.C., Labor, Kuhns, D.B., Blanco, J.C.G., Med Vedeve, R.C., Lentschat, A., Kuhns, D.B., Blanco, J.C.G., Salkowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N.	Bacterial Infections J. Exp. Med. (2003) In press	Distinct Mutations in IRAK-4 Confer Hyporesponsiveness to Lipopolysaccharide and Interleukin-1 in a Patient with Recurrent	Medvedev, A.E., Lentschat, A., Kuhns, D.B., Blanco, J.C.G., Salkowski, C., Zhang, S., Arditi, M., Gallin, J.I. and Vogel, S.N.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (hasea Fo 1301)	Homo sapiens (human) Homo sapiens	AY283670 AY283670.1 GI:31871817	Homo sapiens interleukin-1 receptor associated kinase 4 mutant form 1 (IRAK4) mRNA, complete cds.

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